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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Oct 1 13:52:39 1999; MasPar time 25.13 Seconds 390.202 Million cell updates/sec Run on:

not generated. Tabular output >US-09-026-400-2 (1-461) from US09026400.pep 3223 1 MVHQSNGHGEAAAAANGKS......LERVKSFCQRNKKKNSINGC 461 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part11 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 35.539; Variance 164.075; scale 0.217 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

; ;	Fred. No.	4 566-283	7.136-252	8.256-24	4.95e-13	6.000-13	3 196-09	1 736-08	200.00	1 956-07	1 956-07	1.956-07	2.578-06	3 936-05	4 710-05	70-076	5.64e-05
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		W61642	W61643	424257	W24249	W24252	W22943	W04558	R89906	R89896	R89897	R89898	R35231	¥60239	R25406	421755	R15505
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% Query Match		100.0	89.6	12.5	8.6	8.6	7.2	6.9	6.7	6.5	6.5	6.5	6.1	5.6	5.6	5.5	5.5
Score		3223	2888	403	277	276	231	222	216	209	209	209	195	180	179	178	178
Result No.		٦	7	m	4	'n	9	7	ω	σ	10	11	12	13	14	15	16

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Gaps

0; Indels 0;

Score 3223; DB 34; Length 461; Pred. No. 4.56e-283; 0; Mismatches 0; Indels 0;

Query Match 100.0%; Best Local Similarity 100.0%; Matches 461; Conservative

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1 mvhqsnghgeaaaaangksnghaaaangksnghaaaaavewnfargkdgilattgakns 60

Zucchini ACC synthase 5.64e Protein encoded by zu 6.75e Zucchini ACC synthase 6.75e A human mutant alanin 8.08e Human ALT. Garnation ACC synthas 2.83e Zucchini ACC synthase 4.82e Tomato ACC synthase 4.82e Tomato ACC synthase 6.75e I-aminocyclopropane-1 2.36e hisC gene product of 3.35e Ammonifex histidinol 1.13e Poplar 1-aminocyclopri	Pelargonium 1-aminocy Pelargonium 1-aminocy Crucifer 1-aminocy 10 Grucifer apartate tra Grucifer apartate tra Tomato ACC synthase e 1 ACC synthase E 1 Papaya ACC synthase E 1 Papaya ACC synthase E 1 Tomato ACC synthase e 1 Focoli ACC synthase 5 P.denitrificans COB E Pelargonium 1-aminocy 5 Pelargonium 1-aminocy 5	rt san po
W47311 W47311 W45504 W62504 W62530 W04553 W47312 W15510 W37444 W24715	W60233 W60234 W60234 W5144 W24248 W47312 W47312 W47313 W47313 W67484 W67484 W67506 W47313 W60235	Wel642 standard; Protein; 461 AA. Wel642; 27-OCT-1998 (first entry) Nicotianamine aminotransferase 49564 nicotianamine aminotransferase; plan from deficiency chlorosis. 26-AUG-1998. 21-FEB-1998; 102891. 21-FEB-1998; 102891. 21-FEB-1997; JP-037499. NOWN: S. NARAISHI H, TAKAHASHI.M; WELI 98-439341/38. New nicotianamine aminotransferase penhancing iron absorption of plant colains; page 12-13; 17pp; English. The nicotianamine aminotransferase colains; page 12-13; 17pp; English. The nicotianamine aminotransferase colains in colains as page 12-13; 17pp; English. The nicotianamine aminotransferase colains of the nicotianamine aminotransferase colains of the nicotianamine aminotransferase stransformed cells. The gene fragment and/or isolate nicotianamine aminotry Sequence 461 AA;
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44 44 44 44 44 66 64 64 64 64 64 64 64 6	8 4 4 4 8 4 4 4 8 8 8 9 4 4 8 8 8 9 9 4 8 8 8 8	rd; Protein; 461, (first entry) aminotransferase aminotransferase cy chlorosis. 102891. TP-037499. ONO CHEM CO LTD. 1381. The aminotransfer a bsorption of pi 12-13; 17pp; Engi nine aminotransfer n absorption of pi pi 11-13; 17pp; Engi nine aminotransfer no produce cells wi pi not stated the oproduce cells wi pi not stated the oproduce sis in calcare ells. The gene fare
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New transaminase(s) and aminotransferase(s) derived from host cells

"used for producing enzymes, and hybridisation probes for a CDNA or
genomic library

genomic library

"Institute the sequence comprises aspartate aminotransferase VF5/AA

"This protein and "The VF5/AA amino acid sequence was deduced from genomic aminotransferases (W24248-57) can be produced from native or recombinant host cells for use with L- and/or D-amino acids for production of optically pure chiral compounds used in the production of optically pure chiral compounds used in the pharmaceutical, agricultural and other industries. A method is claimed for transferring an amino group from an amino acid to an alpharketo acid using a claimed enzyme. The measurement of an anino acid to an alpharketo acid using a claimed enzyme. The measurement of an anino acid to an alpharketo acid using a claimed enzyme.
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                                                                                                       HLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIAPVLSIGSLSKSWIVPGWR
                                                                lgwvavydprkilgetkistsitnylnvstdpatfigaalpgilentkedffkaiigllk
                                                                                                                                                                                                                                           Score 403; DB 26; Length 394;
Pred. No. 8.25e-24;
87; Mismatches 145; Indels 26;
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                                                                                                                                                                                                                                                                                                                                        18-FEB-1998 (first entry)
Aquifex aspartate aminotransferase VF5/AA.
Aspartate aminotransferase; VF5/AA; chiral compound.
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MY4257 standard; Protein; 394 AA AC WA257;
DT WA257;
DT WA257;
DT WA5Partate aminotransferation and agailex aspartate aminotransferation and Aspartate aminotransferase; VF5/MOST20187-A1.
PD 14-AUG-1997; U01094.
PP 21-AN-1996; US-56950.
PP 21-AN-1996; US-56950.
PP 08-MAY-1996; US-569171.
PA (RECC-) RECOMBINANT BIOCATALYSIS PI Swanson RV, Warren PV;
DR WPL: 97-415343/38.
DR N-PSDB; T78781.
PT New transaminase(s) and aminotrangen of the producing enzymes, and progenomic library.
PT Genomic library PF Glaim 19; Fig 10; 95Pp; English.
CC Aquifex VF5, a strictly chemocomic library producing enzymes, and prove optimally at 85-90 decomplement and the production of optically pure chicken aminotransferases (W4248-57) cannotransferase (W4248-57) canno
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12.5%;
Best Local Similarity 29.1%;
Matches 106; Conservative
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Claim 3; Page 14-15; J7pp; English.

The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is limplied (though not stated) that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransferase genes.
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Nicotianamine aminotransferase 58148.62 molecular weight protein.
Nicotianamine aminotransferase; plant; iron absorption;
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Pred. No. 7.13e-252;
30; Mismatches 20;
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19-FEB-1998; 102891.
21-FEB-1997; UP-037499.
(SUMO ) SUMITOMO CHEM CO LID.
MOI S, NAKANIShi H, TAKAHAShi M; WPI; 98-439341/38.
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1 Similarity 88.1%;
409; Conservative
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S claim 19; Fig 2: 95pp; English.

This protein sequence comprises aspartate aminotransferase B
(VFS/AAB) of Aquifex VFS, a strictly chemolithoautotrophic, marine
(VFS/AAB) of Aquifex VFS, a strictly chemolithoautotrophic, marine
c with a still medium. The amino acid sequence was deduced from an
isolated genomic DNA sequence (see T78773). Claimed thermostable
transaminases and aminotransferases (W24248-57) can be produced
from native or recombinant host cells for use with L- and/or
C from native or recombinant host cells for use with L- and/or
C b-amino acids for production of optically pure chiral compounds
used in the pharmaceutical, agricultural and other industries. A
method is claimed for transferring an amino group from an amino
c acid to an alpha-ketc acid using a claimed enzyme. The measurement
of aspartate aminotransferase levels in blood serum is used as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 v-thnagekillpdpsypcykn-fayl-ldaqpvfvnv-dketnyevrk-emledidaka 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 VLAQTAGANILLPRPGYPNYEARAAFNKLEVRH-FDLIPDKGWEIDIDSLESIADKNTTA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
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               383 MFVMVKLNLHLLEEIHDDIDFCCKLAKEESVILCPGSVLGMENWVRITFACVPSSLQDGL 442
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fyifpdfsaya-eklggdvklsefllekakvavvpgsafgapgflrlsyalseerlvegi 384
                                                                                                                                                                                                                                                                                                                                   New transaminase(s) and aminotransferase(s) derived from host cells - used for producing enzymes, and hybridisation probes for a CDNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The measurement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 iv-ingfskyfcmpgfrigwmiv-peelvrkaei-v-iqnvf-isa-p-tlsgya-a--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 277; DB 26; Length 373;
Pred. No. 4.95e-13;
92; Mismatches 132; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yefalkllrearvavtpgvdfgknktkeyirfaytrkieelkegverikkf 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998 (first entry)
Aquifex aspartate aminotransferase B (VF5/AAB).
Aspartate aminotransferase B; VF5/AAB; chiral compound.
Aquifex sp. strain VF5.
14-2nr-1.7-1.
                                                                                                                                                                                                                                                                              (RECO-) RECOMBINANT BIOCATALYSIS INC.
SWADSON RV, WAITEN PV;
WPI; 97-415343/38.
N-PSDB; T78773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 8.6%;
Local Similarity 27.9%;
Les 98; Conservative
                                                                                                                                                                                                                           14-AUG-1997.
21-JAN-1997; U01094.
08-MAY-1996; US-646590.
09-FEB-1996; US-599171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 AA;
                                                   rrik 388
                                                                           ERVK 446
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Matches
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14-AUG-1997.
21-JAN-1997; U01094.
80-MAY-1996; US-646590.
80-FEB-1996; US-59911.
87-8-1996; US-59911.
87-8-1997.
87-8-1996; US-59911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pdfdtpehikeaakraldgg-ftkytpvagilplreaiceklyrdngleyspneivvscg
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Alanine aminotransferase. barley; Brassica tugor gene - 26; btg-26 gene; promoter; osmotic stress; stress tolerance; drou nitrogen assimilation; nitrogen metabolism; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 398;
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Pred. No. 6.00e-13;
69; Mismatches 124; Indels
                                                                                                                                                                   Ammonifex degensii aspartate aminotransferase KC4/AA.
Aspartate aminotransferase; KC4/AA; chiral compound.
Ammonifex degensii strain KC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oilseed rape; rapeseed oil; canola.
Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 aaalaalkgpqepvenmrrafqkr 300
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T 5
W24252 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.6%;
Best Local Similarity 23.9%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1998 (first entry)
                                                                                                                                       (first entry)
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14-FEB-1997; CA0100.
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                                                                                                                              18-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                          per construct for expressing enzyme involved in nitrogen assimilation or metabolism in plants - useful to improve stress tolerance, reduce fertilises redemand or increase growth rate tolerance, reduce fertilises redemand or increase growth rate in this protein comprises barley alanine aminotransferase, an enzyme involved in alanine biosynthesis and nitrogen metabolism. A claimed genetic construct (A) for expression in plants comprises a sequence encoding an enzyme involved in nitrogen metabolism. A claimed genetic construct (A) for expression in plants comprises a sequence encoding an enzyme involved in nitrogen as the casmilation/metabolism, and an inducible promoter such as the casmilation/metabolism, and an inducible promoter (see T75511). Also new are: (1) a cloning, expression or plant transformation vector containing (A); and (2) a plant cell transformed with (A), and a plant regenerated from it. (A) is used to transform rape, and a plant regenerated from it. (A) is used to transform rape, containing (A); and (2) a plant cell transform rape, containing (A); and (2) a plant cell transform rape, containing (A); and (2) a plant cell transform rape, containing (A); and (2) a plant cell transform rape, containing in improved agronomic properties, e.g. better stress conting in improved agronomic properties, storage or metabolism of contrainers and plants under nitrogen starved/drought conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 yshsqgikglrdaiasgiasrdgfpanaddifltdgaspgvhlmmqllirnekdgilvpi 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 YAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILLPR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 pgyplysasialhggalvpyylnestgwgletsdvkkqledarsrginvralvvinpgnp 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 40-42; 98pp; English.
Carnation cv. White Sim 1-aminocyclopentane-1-carboxylic acid (ACC)
synthase (W04558) catalyses the initial step of ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing transgenic plants, with reduced climacteric ethylene produ. - to give flowers and buds, specifically carnations, with increased post-harvest life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
9
                                                                                                                                                                                                                                  Genetic construct for expressing enzyme involved in nitrogen assimilation or metabolism in plants - useful to improve stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michael MZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 231; DB 26; Li
Pred. No. 3.19e-09;
38; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 tgqvlaeenqydivkfckneglvlladevy 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 CGSVYSYDHLAKVAEVARKLGILVIADEVY 259
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(FLOR-) FLORIGENE INVESTMENTS PTY LTD.
Cornish EC, Graham MW, Gutterson NI,
                                                                                                                                                          Stroeher VL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%;
Best Local Similarity 30.0%;
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US-599968.
                                                (UTAL-) UNIV ALBERTA.
(GODD/) GODD A G.
(MUEN/) MUENCH D G.
GODD STROPHER V L.
GOOD AG, MUENCH DG, S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1996; AU0286.
09-MAY-1995; AU-002862.
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                                                                                                                                                             Good AG, Muench D0
WPI; 97-425038/39.
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                                                                                                                                                                                     WPI; 97-425038
N-PSDB; T75572
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     14-FEB-1996;
14-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GLPAARSAVAEHLSQGVPYKLSAD-DVFLTAGGTQAIEVIIPVLAQTAGANILLPRPGYP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 vldkátlkmlltfýnak-nihlvcdeíyattvfnspsfisvaevíkdmphvngálvhily 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 glpefrsavakfmgkardekvifnpdrivmsggassasetllfclan-pgdaflipspyyp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 afnrdlrwrtgvnlipftcsssnnfkitkealgsayedalkknikvkgiivtnpsnplgt 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated DNA encoding mammalian kynurenine amino:transferase (KAI) useful in gene therapy applications and for identifying KAI in brain
                                                                                                                                                                                                                                                                                                                         Score 222; DB 20; Length 517;
Pred. No. 1.73e-08;
91; Mismatches 136; Indels 33; Gaps
biosynthesis in the plant. Its amino acid sequence was deduced from a full-length gene (738896). Expression of a nucleic acid (738897) conding for a fragment (W04559) of the ACC synthase in transgenic carnation reduces the formation of ACC synthase by co-suppression. The reduction in ACC synthase activity results in decreased climacteric ethylene prodn. by the plant and hence delayed senescence of flowers and buds after cutting, and increased Sequence 517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human kynurenine aminotransferase (KAT).
Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KYN; brain; NMDA receptor; glutamatergic function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 lwrviinevkinvspgssflcsepgwfrvcfanmdnatldvalnrirsfvtrgrvdns 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 slskdmgmpgfrvgilysyn-drvvstarrmssf-g-l-vssq-tqfmlaallsdddfvr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 ADFFKRIIG-LLKESSEICYREIKENKYIICPHKPEGSMFVMVKLNLHLLEEIH-D-DID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 r-flvesrdrlfrrhqhft-sel-akigigclq-gnaalfvwmdlr-hlldeatverelk
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23-JUN-1995: U07855.
07-JUL-1994; US-271667.
(PRAA.) PHARMACIA SPA.
(UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mosca M,
                                                                                                                                                                                                                                                                                                                                   7 Match 6.9%;
Local Similarity 27.4%;
Les 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R89906;
15-JUL-1996 (first entry)
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168 lgasndwqldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcgqhdvvcisd 227
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Sequences encoding Kynurenine aminotransferase (KAT) can be inserted into vectors and subsequently cells and hence can be used for gene therapy. The vector and host cells can be used for cerebral implantation to where KAT can directly catalyse the production of kynurenic acid (KYNA) from Kynurenine (KYN). It is thought KYNA acts as a negative endogenous modulator of cerebral glutamatergic function. KYNA concentrations and the activity of KAT show an increase with age. KAT inhibitors, by providing an increase of the slutamatergic tone at the NMDA receptor, could be useful in situations where NMDA receptor function is insufficient and/or KAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) - useful in gene therapy applications and for identifying KAT in brain
                Rat kynurenine aminotransferase (KAT) clone.
Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KYN; brain; NMDA receptor; glutamatergic function.
Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity and KTNA levels are abnormally enhanced. Hence they could be particularly useful in the treatment of the parhological consequences associated with the aging processes in the brain. Three KAT clones are described in 711560, 711742-43.
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KYN; brain; NMDA receptor; glutamatergic function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 209; DB 17; Length 437;
Pred. No. 1.95e-07;
24; Mismatches 46; Indels
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Rat Kynurenine aminotransferase (KAT) clone.
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23-JUN 1995; UO7855.
27-JUL 1994; US-271667.
(PHAA ) PHARMACIA SPA.
(UXMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA SPA. (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                       Mosca M,
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larity 33.0%;
Conservative
                                                                                                                                                                  25-JAN-1996.
23-JUN-1995; U07855.
07-JUL-1994; US-271667.
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nes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 96-097623/10.
N-PSDB; T11742.
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N-PSDB; T11743.
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WO9601893-A1.
                                                                                                                                        WO9601893-A1.
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                                                                                                                                                                                                                                                                                                                                    192 VRHFDLIPDKGWEIDIDSLESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 lgasndwgldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcgghdvvcisd 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 LIPDKGWEIDIDSLESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIAD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) - useful in gene therapy applications and for identifying KAT in brain
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kynurenine aminotransferase, KAT; kynurenic acid; KYNA; kynurenine; KYN; brain; NMDA receptor; glutamatergic function.
consequences associated with the aging processes in the brain. This is the human RAT sequence. Three rat KAT clones are described in Til560, Til742-43. Sequence 422 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                            Ή;
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Pred. No. 1.95e-07;
24; Mismatches 46; Indels
                                                                                                                                                                     Length 422;
                                                                                                                                                           Score 216; DB 17; Length 42
Pred. No. 5.30e-08;
29; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 vcitdevyqwmvydghqhisiaslpgmwertltigsagktfsatgwkvgwv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| || :::: : : | ::|| || :::|| || EVYGKLVLGSAPFIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 evyqwlvydghqhvsiaslpgmwdrtltigsagksfsatgwkvgwv 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwarcz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat kynurenine aminotransferase (KAT) clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mosca M, Okuno E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Figure 2; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 9
R89896 standard; Protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          л 10
R89897 standard; Protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PHAA ) PHARMACIA SPA. (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                              Similarity 30.68;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
Local Similarity 33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1995; U07855.
07-JUL-1994; US-271667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benatti L, Breton J,
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96-097623/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T11560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1996.
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                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ysissgiqpiredvaqyierrdggipadpnniflstgasdaivtmlkllvsgegrartgv 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 lipipqyplysaalaeldavqvdyy-ldeerawaldiaelrralcqardrccprvlcvin 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 lgasndwqldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcqqhdvvcisd 247
kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts as a negative endogenous modulator of cerebral glutamatergic function. KYNA concentrations and the activity of KAT show an increase with age. KAT inhibitors, by providing an increase of plutamatergic tone at the NWDA receptor, could be useful in situations where NWDA receptor function is insufficient and/or KAT be particularly useful in the treatment of the pathological consequences associated with the aging processes in the brain. Finee KAT clones are described in T11560, T11742-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human alanine-amino-transferase gene fragments - used as marker in diagnosing hepatic diseases
Disclosure; Page 11-13; 15pp; Japanese.
The sequences given in R35230-31 represent human and rat alanine aminotransferase (ALT) genes respectively. ALT is an important marker in the diagnosis of hepatic disease. Gene fragments of ALT can be used in inexpensive, large scale production of human ALT which can then be used as a standard in the determination of human Serum ALT. See also Q40500-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer; polymerase chain reaction; PCR; amplify; human; diagnosis; alanine aminotransferase; ALT; marker; hepatic disease; serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 457;
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Pred. No. 2.57e-06;
42; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 209; DB 17; Length 45
Pred. No. 1.95e-07;
24; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 evyqwlvydghqhvsiaslpgmwdrtltigsagksfsatgwkvgwv 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 EVYGKLVLGSAPFIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1991; 222318.
06-AUG-1991; UP-22318.
(KAGAR ) KAGAKU OYOBI KESSEI RYOHO KENKYUSHO.
WPI; 93-136892/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | || || | | : : : | | | | | ::::||||| | PNNPCGSVXSYDHLAKVAEVARKLGILVIADEVX 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pgnptggvqtrecieavirfafkeglflmadevy
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W60239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 12
R35231 standard; Protein; 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.1%;
Best Local Similarity 29.2%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.5%;
Best Local Similarity 33.0%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R35231;
10-AUG-1993 (first entry)
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J05068548-A.
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RES
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28-SEP-1998 (first entry)
Rose 1-aminocyclopropane-1-carboxylase synthase.

EARD

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New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced a rose, used to develop products for producing plants with reduced a rose, used to develop products for producing plants with reduced a rose, used to develop. Fightish.

Claim 60; Fig 10: 77pp; English.

This amino acid sequence of this 1-aminocyclopropane-1-carboxylate synthase of ACC synthases of rose cv. Red Cardinal was deduced from isolated CDNA clone pRosekac7 (see V30330). The invention relates to new isolated ACC synthase genes from geranium and rose (see V30324-26 and V30330) and the use of antisense fragments of these creek coontrol expression of ACC synthase genes in transgenic plants, especially in geranium, rose and woody plants. By reducing the amount of ACC synthase produced in plant cells, the rate of ACC conversion to ethylene can be decreased. This can be used to prolong the shelf-life of cut flowers and to reduce leaf yellowing and betal abscission during shipping and storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Without induced ACC synthetase gene - used for control of bio-synthesis of ethylene, for controlling growth, maturity and ageing of higher plant ageing of higher plant.

Claim 2; Fig 1; 10pp; Japansee.

Claim 2; Fig 1; 10pp; Japansee.

Chacly synthetase (EC 4.4.1.14) which was obta. by screening a cDNA concoling detriment induced 1-aminocyclopropane-1-carboxylic acid (ACC) synthetase (EC 4.4.1.14) which was obta. by screening a cDNA library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from cDNA library clones was screened by an antibody method to identify colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/pb/WW33.

CBlosynthesis of ethylene is controlled by ACC synthetase. Ethylene controls the growth, maturing and aging of higher plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geelgisgiacygpsdglmelklavagfmskaignsvtynpsgivltagatpaleilsfc 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 lads-gnaflvpapyypgldrdvkwrtgveiipvpcrsadkfnlsitaldrafngakkrg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 180; DB 32; Length 480;
Pred. No. 3.93e-05;
50; Mismatches 70; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 vkvrgiiisnpsnpggslltreslynlldfareknihiisnelfagstygseefvsma 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 AMV---II-NPNNPCGSVYSYDHLAKVAEVARKLGIIVIADEVYGKLVLGSAPFIPMG 273
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ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
ethylene; transgenic plant; wilting; rose; pRoseKacc7.
Rosa sp. cv. Red Cardinal.
W09814465-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ethylene; growth; maturity; aging; plant.
Cucurbita maxima.
                                                                                                                                                                                                                        01-OCT-1996; US-724194.
(COLS ) UNIV COLORADO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
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R25406 standard; Protein; 493
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31-OCT-1990; JP-296943.
(SUMO ) SUMITOMO CHEM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 5.6%;
Local Similarity 27.0%;
Les 48; Conservative
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                                                                                                                                                                                  30-SEP-1997; U17644
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                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V30330
                                                                                                                                                    09-APR-1998.
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       NAME OF THE PROPERTY OF THE PR
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25;
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Claim 2: Pages 9-11: 12pp; Japanese.
This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase
encoded by a cDNA clone isolated from poplar trees which
had been exposed to corone. Exposure conditions were: 0.1 ppm ozone
for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
humidity, 30 k lux and air current 30 cm/second. The gene will be
useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                   215
                                                                                                                                                                                           \verb"ttydrdtlktlvtfvnqhdihlicdeiysatvfkaptfisiaqiveemehckkelihilg" 275
                                                                glpefrngiasfmgkvrggrvqfdpsrivmgggatgasetvifclad-pgdaflvpspyy 155
                                                                                      276 slskdmglpgfrvgilysyndv-vvrrargmssf-g-1-vssqtqhllaamlsd--edfv 329
                                                                                                                                                                                                                                                                             330 dkflaenskrlaerharftkel-dkmgitclnsnag-vfvwmdlr-rilkdqtfkaemel 386
                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glpefrqaiakfmgrvrggrvtfdpdrivmsggatganelimfclad-pgdaflvpspyy 149
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                                                                                                                            aafdrdlkwrtraqiirvhcnssnnfqvtkaaleiaykkaqeanikvkgviitnpsnplg
                                                                                                                                                                                                                  32 SVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMG--V--FGHIAPVL-SIG-
                                                                                                                                                                                                                                                                                                                                               346 ADFFKRIIGLLKESSEICYREIKENKYIICPHKPEGSMFVWVKLNLHLL-EE-1HDDIDF
                                                                                                                                                                                                                                                                                                                                                                                      387 wrviinevklnvspgssfhvtepgwfrvcfanmddntvdvalnrihsfvenidkke 442
                                                                                                                                                                                                                                                                                                                                                                                                            (Note: Record has been revised in order to correct the Organism Source field).
   Score 179; DB 5; Length 493;
Pred. No. 4.71e-05;
95; Mismatches 143; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ozone-induced 1-amino: cyclopropane-1-carboxylic acid synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1997 (revised)
26-AUG-1997 (first entry)
Poplar 1-aminocyclopropane-1-carboxylic acid synthase PNACCS2.
Ozone, induction; exposure, resistance; transgenic plant; ACC;
1-aminocyclopropane-1-carboxylic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 23; Length 486;
Pred. No. 5.64e-05;
98; Mismatches 143; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .r 15
W21755 standard; Protein; 486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR 1997.
07-SEP-1995; 254510.
07-SEP-1995; JP-254510.
(TOYT ) TOYOTA JIDOSHA KK.
WPI; 97-239270/22.
Query Match
Best Local Similarity 24.7%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.5%;
Best Local Similarity 24.5%;
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T73502
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J09075088-A.
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ttldretlkcllsfineknihivcdeiyaatifssqnfvsvsevieevmdcnrdlihivy 269
                  324 edflaesskrikkrhgiftkgleqig-iscleskag-lfvwmnlr-hilkeqtndgemel 380
                                                                                                                                                  346 ADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVMVKLNLHLL-EEIHD-DIDF 403
                                                                                                                                                                               381 wrvivndvklnvspgssfhcvepgwfrvcfanmddetlevalkrihafvgegkeretls 439
                                                                                                                                                                                                  slskdmglpgfrvgivysynda-vvncgrkmssf-g-l-vssq-tqyllasmlsd-eefv
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Search completed: Fri Oct 1 13:53:16 1999 Job time : 37 secs.

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179066 seqs, 54579741 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 49.304; Variance 91.106; scale 0.541 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.31e-248	1.33e-123 1.44e-75	3.71e-68	. 69e-63	11e-57	3.15e-56	8.18e-56	3.06e-50	.20e-49	2.14e-48	.41e-47	03e-43	3.75e-41	.02e-40	1.29e-35	68e-34	2.65e-34	1.17e-34
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Description	TYROSINE TRANSAMINASE-	F4ZD1.Z PROTEIN. ASPARTATE AMINOTRANSFE	PUTATIVE AMINOTRANSFER	ASPARTATE AMINOTRANSFE	FROM BASES 2401667 TO	ASPARTATE AMINOTRANSFE	PUTATIVE AMINOTRANSFER	SOLUTE-BINDING SIGNATU	HYPOTHETICAL 39.5 KD	ASPARTATE AMINOTRANSFE	PUTATIVE AMINOTRANSFER	AMINOTRANSFERASE.	391AA LONG HYPOTHETICA	ASPARTATE AMINOTRANSFE	389AA LONG HYPOTHETICA	ASPARTATE AMINOTRANSFE	ASPARTATE AMINOTRANSFE	ASPARTATE AMINOTRANSFE
ΩI	049451	033267	086587	P71348	P77727	067781	088124	025383	005237	060013	053870	054170	058489	028151	059096	033822	056232	027916
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% Query Match Length	389	404 429	402	404	405	394	402	390	357	397	397	382	391	379	389	383	385	374
% Query Match	39.6	15.4	14.3	13.5	12.7	12.5	12.4	11.6	11.4	11.3	11.2	10.6	10.2	10.0	9.3	9.5	9.5	9.1
Score	1275	495	460	4 4 35	410	403	401	374	368	365	361	342	330	323	299	296	295	294
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ASPARTATE AMINOTRANSFE 2.56e-33 PUTATIVE ASPARTATE AMI 6.08e-32 AMINOTRANSFERASE (ASPC 9.05e-31 HYPOTHETICAL PROTEIN 6.09e-29 R03A10.4 PROTEIN. 1.56-27 ORFT. 1.56-27 HYPOTHETICAL 16.7 KD P 1.05e-26 ASPARTATE AMINOTRANSFE 1.05e-26 ASPARTATE AMINOTRANSFE 1.05e-26 ASPARTATE AMINOTRANSFE 1.05e-26 ASPARTATE AMINOTRANSFE 1.05e-25 ACC STUTHASE 1.05e-22 ALANINE AMINOTRANSFERA 1.05e-22 ALANINE AMINOTRANSFERA 1.02e-19 GLUTAMINE-PHENYLPYRUV 3.50e-19 GLUTAMINE-PHENYLPYRUV 3.50e-19 GLUTAMINE-PHENYLPYRUV 1.02e-17 YDED PROTEIN 1.02e-17 YDEF PROTEIN 1.55e-17 1-AMINOCYCLOPROPANE-1 8.23e-17 1-AMINOCYCLOPROPANE-1 8.23e-17 HYPOTHETICAL 44.4 KD P 2.86e-16 HYPOTHETICAL 44.4 KD P 2.86e-16 HYPOTHETICAL 55.0 KD P 2.86e-16	ss.	TED) SEQUENCE UPDATE) ANNOTATION UPDATE) IN (EC 2.6.1.5)	<pre>; THALIANA (MOUSE-EAR CRESS). VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; TES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; BRASSICACEAE; ARABIDOPSIS.</pre>	SEQUENCE FROM N.A. SEQUENCE FROM N.A. BEYAN M., KOETTER P., HEMPEL S., ENTIAN KD., HOHEISEL J., MEWES H.W., MAYER K., SCHUELLER C.; SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. EU ARABIDOPSIS SEQUENCING PROJECT; SUBMITTED (APR.1998) TO EMBL.GENBANK/DDBJ DATA BANKS. -! - CATALYTIC ACTIVITY: L-TYROSINE + 2-OXOGLUTARATE = 4-HYDROXYPHENTLDYROVATE + L-GLUTAMATE. -! - COFACTOR: PYRIDOXAL-PHOSPHATE. EMBL; ALO21749; E1250059; TRANSFERASE; AMINOTRANSFERASE. SEQUENCE 389 AA; 43018 MW; D4BCDB9F CRC32;	e 1275; DB 10; Length 389; I. No. 2.31e-248; Mismatches 93; Indels 6; Gaps 6;	TQTQDETDISVWRF-RGSDNA-ARASS-VIMRVIVYKLEDECSLDVKKPLLPLAHGDPSV 72 : : : ::: :: : SNGHAAAAAVEWNFARGKDGILATTGAKNSIRAIRYKISASVEESGPRPVLPLAHGDPSV 90	PCYRTSILVENAVVDVLRSGKGNSYGBAAGILPARQAVADYVNRDLTNKVKPNDVFITV 132 : :: : : : ::: : : : PAFRTAVEAEDAVAAALRIGGENCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTA 150	GCNOGIEVVLOSLAR-PNANILLPRPSYPHYEARAVYSGLEVRKPDLLPFKEWEIDLPG1 191 - : :
028650 086459 086459 0868459 0868473 086873 086873 081658 081658 081658 081658 081658 081658 081658 081668 081668 081668 081668 081668 081668 081668 08168 0	IGNM	REAJ	E-EAR CI STREPTOI YTA; MAK ARABIDOI	EL S., 1 ELLER C BL/GENBA	PROJECT BL/GENBA TYROSINI E + L-G OSPHATE ASE.	Score Pred. 89;	-RGSDNA-AKASS-' 	KGNSYGP :: QFNCYAA	LLPRPSY : LLPRPGY
100 110 4 2 110 100 100 100 100 100 100 100 100 1	,	06 06 07 IIKE	ACUS AE; FOPH AE;	HEMP SCHU	ING DEM TVAT L-PH 59;	. 56.8; 1.08;	SDNA KDGI	LRSG : LRTG	NANI GANI
39 48 48 48 48 48 48 48 48 48 48 48 48 48		049451; 049451; 01-JUN-1998 (TREMBLREL. 06, C 01-JUN-1998 (TREMBLREL. 06, I 01-AUG-1998 (TREMBLREL. 07, I TYROSINE TRANSAMINASE-LIKE PR (TYROSINE AMINOTRANSFERASE).	F2109.100 ARABIDOPSIS THALIANA (MOUSE EUKARYOTA; VIRIDIPLANTAE; S EUPHYLLOPHYTES; SPERMATOPHY CAPPARALES; BRASSICACEAE; P	.A. ER P., 1 ER K., 3	12) EQUENCE FROM N.A. EU ARABIDOPSIS SEQUENCING PRO- SUBMITTED (APR-1998) TO EMBLA -!- CATALYTIC ACTIVITY: L-TYR -!- COFACTOR: PYRIDOXAL-PHOSPI EMBL; ALO21749; E1250059; EMBL; AMONTANSERASE SEQUENCE 389 AA; 43018 MW;	h Similarity 47.5% 170; Conservative	VWRF-RG EWNFARG	ENAVVDV : EDAVAAA	QSLAR-P :: PVLAQTA
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		PKE 998 (TR) 998 (TR) 998 (TR) TRANSA). SIS THAN A; VIRI) PHYTES; ES; BRA	FROM N KOETT	FROM N DOPSIS O (APR- STTIC A DROXYPH CTOR: P D21749; ASE; AM	Similar 70; Co	TQTQDETDISVWRF : : : SNGHAAAAAVEWNF	FRTSILV : :: FRTAVEA	GGIEVVL : :: QAIEVII
200333445419888438000000000000000000000000000000000		9451; -JUN-19 -JUN-19 -AUG-19 ROSINE	F2109.100 ARABIDOPS EUKARYOTA EUPHYLLOP	OUENCE SVAN M. SWES H.	[2] SEQUENCE SUBMITTEI - ! - CATAI - ! - COFAC EMBL; AL(TRANSFERZ SEQUENCE	Matc Local	16 TQT(: 31 SNG	73 YPC' : 91 FPA	133 GCN
77777777777777777777777777777777777777			CCCCS	S WE SE	RRN 128 RRP SEC CC - 1 CCC - 1 CCC - 1 SQ SE SQ SQ SE SQ	Query l Best L Matches	Oy Oy	Db Qy	Db 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIAKRWMYPGWRLGWLIIHNHFGVLTDVKNGI-VALSQKI-VGPCSLVQGALPKILRETP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 SLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 VLPQSAHSKNTVNPVR-KIADACAVPPHPEKKVIKLHLGDPSVGGKLPPSEIAVQAMHES 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSSHMFDGYGPAVGALAAREAIVERYS-SADNVFTADDVVLASGCSHALQMAIEAVAN-A 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDYFVYTRNVIETNANIVDSILADVPGMRVV-KPKGAMYMMVNIS-R--TAYGSDVSFCQ 394
EAMADENTVAMVIINPNNPCGNVYSYDHLKKVAETAKKLGIMVITDEVYCQTIFGDKPFV 251
                                                                  PMGEFSSITPVITLGGISKGWIVPGWRIGWIALNDPRGILKSTGMVQSIQQNLDITPDAT 311
                                                                                    MEDLINE; 94150718.
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MEDRIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A., CONSTILL M., DEAR S., DU Z., DURRIN R., FAVELLO A., FULTON L., JONES M., KERSHAW J., KIRSTEN T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LATSTER M., LATREILLE P., LIER M., JOHNSTON L., LIGHTNING J., LOOPE, C., MCMRRAY A., MORTIMORE B., O CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R. SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., HOMAS K., VAGDIN M., VAGGHAN K., WATERSTON R., WATERSTON R., WATERSTON R., WATERSTON P., THERMAL MED. MILKINGON-SPROAT J., WOHLDMAN P.; C., RIFKEN L., WALKINGON-SPROAT J., WOHLDMAN P.; C., CONTIGUOUS NUCLEOFIE'S EQUENCE FIRM CHLOMOSOME III Of C.
                                                                                                                                    312 TIVQAALPEILGKANKELFAKKNSMLKQNVELVCDR-LKEIPCLVCNKKPESCTYLLV 368
                                                                                                                                                    EUKARYOTA, METAZOA; NEMATODA; SECERNENTEA; RHABDITIA, RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGHTNING J.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.5%; Score 726; DB 5; Le 30.4%; Pred. No. 1.33e-125; rative 121; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; E1346662; -.
464 AA; 51031 MW; A2E3EAB3 CRC32;
                                                                                                                                                                                                                                        464 AA.
                                                                                                                                                                                                                                          PRT;
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03,
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                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                         01-FEB-1997 (TREMBLREL.
01-FEB-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 368:32-38(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             F42D1.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 281081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEQRDIAWTKLNEIPGVSCV-KPAGALYAFPRLDPEVYD-IDDDEQLVLDLLLSEKILVT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 -LSARRAVVIRYELVPGFP-RFDVDDVYLGNGVSELIIMTLQALLDN-GDQVLIPSPDYP 155
MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKA-DFFKRIIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IRGPVHQHAARLEAEGHR-ILKLNIGNPAPF-GFEAPDVIMRDIIQALPYAQGYSDSQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILTOMYDLARKHOLLLLADEIYDKILYDDAKHISLASIAPDMLCLTFNGLSKAYRVAGYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 429;
                                                                                                                      395 NLIREESVF-CLPGQAFSAPGYFRVVLTCGSEDMEEAALRIREFCYRN 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.G., RAJANDREAM M.A.;
TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO EMBL/GENBANK/DDBJ DATA BANKS
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL: 297991; E330321; -.
PFAM; PF00155; aminotran.l.; 1.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 429 AA; 47350 MW; 9B68011A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.44e-75;
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Best Local Similarity 29.5%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ASPARTATE AMINOTRANSFERASE
                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL.
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SUBMITTED (JUL-1997) 1
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01-JAN-1999 (TREMBLREL.
401AA LONG HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 VAQRY-QALGLEVDVDDVFLGNGVSELISMAVQALLE-DGDEVLIPAPDFPLWTAVTTLA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGKAVHY-LCDEQAEWYPDLADMEAKITDR-TKAVVIINPNNPTGAVYPKEIVEGILDLA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRHGLMVLADEIYDQILYDDAVHHSAASLAPDLVVLTFCGLSKTYRVAGFRSGWLVVTGP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 KQHARDYLEGLIMLASMRLCANAPAQYAIQAALGGR-QSIR-EL-TAPGGRLHEQRDVAW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKILEKTKISTSITNYLNVSTD-PATF-VQEALPKILENTKADFFKRIIGLLKESSEICY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ANALEEAG-HSVLRLNTGNPALF-GFEAPEEIVQDMIRMLPRAH-G-YTDSRGILSARRA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;
A set of ordered cosmids and a detailed genetic and physical map in the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. MICROBIOL. 21:77-9196).
EMBL; AL031514; E1319222;
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 402 AA; 44448 MW; 185FB18E CRC32;
                                                                                                                                                                                                                                                                                                  STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 460; DB 2; Length 402;
Pred. No. 3.71e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
OLIVER K., HARRIS D.;
SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.G., RAJANDREAM M.A.;
TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE;
LAST ANNOTATION UPDATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
1D 05904 PRELIMINARY; PRT; 401 AA.
1C 059044.
DI 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 REIKENKYITCPHKPEGSMFVWVKLNLHLLEBIHDDIDF 403
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                                                                                                                                           402 AA
                                                                                                                                           PRT;
                                                                                                                                                                               01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, PUTATIVE AMINOTRANSFERASE.
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Local Similarity 27.7%;
les 94; Conservative
                                                                                                                                           PRELIMINARY;
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PARKHILL J., BARRELL
SUBMITTED (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE; 97000351.
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390 QGT 392
                                              417 PGS 419
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ID 086587

OT 01-000-11

DT 01-000-12

DT 01-000-12

DE PUTALL O4(000)

OC BACTERIA

OC BACTERIA

OC ACTINOMY.

RN [1]

RP SEQUENCE

RC STRAIN-A

RA OLIVER K

RL SUBMITTE

RN [2]

RP SEQUENCE

RC STRAIN-A

RA PARKHILL

RL SUBMITTE

RN [3]

RP SEQUENCE

RC STRAIN-A

RA PARKHILL

RN [3]

RP SEQUENCE

RC STRAIN-A

RA PARKHILL

RN [3]

RP SEQUENCE

RC STRAIN-A

RA REDENBAC

RA REARRERES

RO REGUENCE

RA REMBAC

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Matches
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RX SEVELINE. 98344137.

RX MEDLINE; 98344137.

RA RAMRABEARASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,

RA RAMRABEARASI Y., SAWADA M., HORIKAWA H., HOSOYAMA A., NAGAI Y.,

RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,

RA SARAI M., OGURA R., NAKAZAWA H., TARAMIYA M., OHUNU Y.,

RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,

RA AOKI K., NAKAMURA Y., ROBE T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,

RA AOKI K., NAKAMURA Y., ROBE T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,

RT "Complete Sequence and Gene Organization of the Genome of a

RT "Complete Sequence archaebacterium, Pyrococcus horikoshii OT3.";

RL HYPET-thermophilic Archaebacterium, Pyrococcus horikoshii OT3.";

KL DNA RES. 5:55-76(1998).

DR EMBL: APONONO6: D1031371; -.

KW TRANSFERASE; AMINOTRANSFERASE.

SO SEQUENCE 401 AA; 45564 MW; O1CD3533 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 REKEKNGVDITPDDVRVTAAVTEALQLIFGALLD-PGDEILIPGPSYPPYTGLVKFYGGK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                              PYROCOCCUS HORIKOSHII.
ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILIE: 95350630.

PLEISCHANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., EULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D., SOOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SADDEK D.M., BRANDON R.C., FINE I.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LEKKGIK-VIRLNIGDPVKF-DFQPPEHMKEAYCRAIQEGH-NYYGDSEGLIELREAIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 PVEYRTIEEEGWQPDIDDLRKKISER-TKAIAVINPNNPTGALYDKKTIEEIINVAGEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 SEVREAIDKLARIRICPNTPGQFA--ALAG-LIGSM-DYLKEYMKKLKERRDFIYKRLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 LVVLSDEIYDLMTYEGKHISP-GSLTKDVPVIVMNGLSKVYFATGWRLGYMYFVDPEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.0%; Pred. No. 9.70e-64;
Matches 90; Conservative 83; Mismatches 135; Indels 1
09, LAST ANNOTATION UPDATE) ASPARTATE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (ASPO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 IPGIS-TTKPQGAFYIFPRIE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LT 6 PRELIMINARY; P71348, 01-FEB-1997 (TREMBLREL. 0 01-FEB-1997 (TREMBLREL. 0 01-NOV-1998 (TREMBLREL. 0
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ESCHERICHIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 KESSEICYREIKENKYITCPHKPEGSMFVWVKLNLHLLEEIHDDIDFCCKLAKEESVILC 416
                                                                                                                                  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAYAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENLAYAGE A.R., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIELEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRAKNN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                             17 IRGPVHKEALRLEEEGNK-ILKLNIGNPAPF-GFEAPDEILVDVLRNLPSAQ-G-YCDSK 72
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 GWVAVYDPTKILEKTKIST-SITNYLNVSTDPATFVQEALPKILENTKA-DFFKRIIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYSARKAIVQYYQSKGI-LGATVNDVYIGNGVSELITMAMQALLN-DGDEVLVPMPDYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 LWTAAVTLSGGKAVHY-LCDEDANWFPTIDDIKAKVNAKTKAIVIINPNNPTGAVYSKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 LQEIVEIARQNNLIIFADEIYDKILYDGAVHHHIAALAPDLLTVTLNGLSKAYRVAGFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWMILNGP-KHNAKGYIEGLDMLASMRLCAN-VP-MQHAIQTALGGYQSINEFILPGGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                    85; Mismatches 159; Indels 16;
           "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd ^{\prime\prime},
                                                                        BROWN N.P., HAYES W.
                                                                                                                                                                                                                                                                                                                                                                           Length 404;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SUBMITTED (SEP-1996) TO EMBL,/GENBANK/DDBJ DATA BANKS.
EMBL, U32714; G1573250; -.
PPRAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 404 AA; 45160 MW; 8082209D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FROM BASES 2401667 TO 2412529
(SECTION 208 OF 400) OF THE COMPLETE GENOME (SECTION 208
                                                                                                                                                                                                                                                  SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                          Score 435; DB 2;
Pred. No. 6.69e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405
                                                             SEQUENCE FROM N.A.
L TATURON R., MUSHEGIAN A.R., BORK P.,
BORDODOVSKY M., RUDD K.E., KCONIN E.V.;
CURR. BIOL. 6:279-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.5%;
Best Local Similarity 28.2%;
Matches 102; Conservative
                                     SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 HG 366
                                                                                                                                                                                                                                         VENTER J.
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P77727
P77727;
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AIBA H., BEBA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMURA S., KITAGANA M., MAKINO K.,
MASUDA S., MIKI T., MIZOBUGHI K., MORI H., MOTOMURA K., NAKANURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEXI Y.,
NASHIMOTO H., TISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEXI Y.,
SUBMITIED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000318; G1788627; -
EMBL; AE000318; G1789660; -
EMBL; D90860; G1799660; -
TRANSFERRASE; AMINOTRALEALI; I.
TRANSFERRASE; AMINOTRANSFERRASE.
SEQUENCE 405 AA; 45517 MW; DF062CD9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 GLYSARKAIMQHYQARGMR-DVTVEDIYIGNGVSELIVQAMQALLNS-GDEMLVPAPDYP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.11e-57;
94; Mismatches 154; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 IRGPVLKEAKRLEEEGNK-VLKLNIGNPAPF-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMEIVEIARQHNLIIFADEIYDKILYDDAEHHSIAPLAPDLLTITFNGLSKTYRVAGFRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 LWIAAVSLSSGKAVHY-LCDESSDWFPDLDDIRAKITPRTRGIVIINPNNPTGAVYSKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GWMVLNGPKK-HAKGYIEGLEMLASMRLCANVPAQHAIQTALGGY-QSI-SEFITPG-GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 GWVAVYDPTKILEKTKIST-SITNYLNVSTD-PATF-VQEALPKILENTKADFFKRIIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYEQRNRAWELINDIPGVSCV-KPRGALYMFPKIDAKRFN-IHDDQKMVLDFLLQEKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 405;
                                          BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
                                                                                          SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL. 07, C
(TREMBLREL. 07, I
(TREMBLREL. 08, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 12.7%;
Local Similarity 27.3%;
hes 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASPARTATE AMINOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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01-AUG-1998 (
01-NOV-1998 (
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PFAM; PF00155
HYPOTHETICAL
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025383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHL-SQG-VPYKLSADDVFLT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 AGAKMVLFLIFMAILDE--GDEVLLPSPYWVTYPEQIRFFGGVPV-EVPLKKEKGFQLSL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 EDVKEKVTER-TKAIVINSPNNPTGAVYEEEELKKIAEFCVERGIFIISDECYEYFVYGD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKFVSPASFSDEVKNITFTVNAFSKSYSMTGWRIGYVA-C-PEEY-AKV-IA-SLNS-QS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VS-NVITFAQYGAL-EALKNPKSKDFVNEMRNAFERRRDIAVEELSKIPGMDVV-KPEGA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 PDFDTPDFIKEACIRALREGKTK-YAPSAGIPELREAIAEKLLKENKVEYK-PSEIV-VS 98
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                                                                                                                                         STRAIN-YF5;
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
CREAHAM D.E., OVERBER R., SNEAD M.A., KELLER M., AUJAY M., HUBER I
FELLDMAN R.A., SHORF J.M., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AEO00766; G2984217; -.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 394 AA; 43777 MW; B9D83011 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; STREPTOMYCES STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;
TRANSTIPION TEQUIALORS.";
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ0055198; E1318411;
EMBL; AJ005198; E1318407; -.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 402 AA; 44414 MW; 5CD3256A CRC32;
   the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Mismatches 145; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 401; DB 2; Length 402;
Pred. No. 8.18e-56;
94; Mismatches 152; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 403; DB 2;
Pred. No. 3.15e-56;
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larity 26.7%;
Conservative
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Local Similarity 29.1%;
les 106; Conservative
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01-NOV-1998 (TREMBLREL. 06
PUTATIVE AMINOTRANSFERASE.
                                                          NATURE 392:353-358(1998)
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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   complete genome
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Best Local Similarity
197; Conser
                                                                                                                     SEQUENCE FROM N.A.
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088124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                 138 SGGKAVHYVCDEAADWYPDLDDMASKITDQTKAVEIINPT---GAVYPKEILEGILDLAR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINEIPGVSCV-KPKGALYAFPRLDPKV-HPIHDDEKFVLDLLLQEKIQVVQGT--GF-N 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.A.,
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SOLUTE-BINDING SIGNATURE AND MITOCHONDRIAL SIGNATURE PROTEIN (ASPB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLEISCHMANN R.D., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A LOFTON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCATRE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M. COTTON M.D., WEIDMAN J.M., FUULI C., BOWMAN C., WAITHEY L., WALLIN HAXES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.
                                                                                                                                        248 KLGILVIADEVYGKLVLGSAPFIPMGVFGHIAPVLSIGSLSKSWIVPGWRLGWVAVYDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the gastric pathogen Helicobacter pylori[published erratum appears in Nature 1997 Sep 25.389(649):412].";
NATURE 388:539-547(1997).
EMBL; AE000580; G2313794; -.
                                                                                                        VAQRYQALGLD-EVSVDDVFLGNGVSELVTMAVQALLE-DGDEILIPAPDFPLWTAVTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
HELICOBACTER.
24 ANALEEAG-HSVLRLNTGNPALF-GFEAPEEIVQDMIRMLPQAH-G-YTDSRGVLSARRA
                                                                                                                                                                                                                                                                                                                                                                                                                                            QHARDYLEGLIMLASMRLCPNAPAQFAIQAALGGR-QSIR-EL-TAPGGALHEQRDRAWE
                                                                                                                                                                                                                                                       RHGLMVFADEIYDQILYDDAVHHSVAALAPDLVVLTFCGLSKTYRVAGFRSGWLVITGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 374; DB 2; Le
Pred. No. 3.06e-50;
85; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42874 MW; BAD53859 CRC32;
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larity 26.7%; Pred. No. 3
Conservative 85; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00155; aminotran_1; 1. HETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 AA;
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nes: 97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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MEDLINE; 97394467
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KUNST F., OGGSAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
A ZEVEDO V., BERTERE M.G., BESSIERES P., BOLOTIN A., BORGHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
BROUILLET S., BRUSCHI C.V., CALDWELL B., CADJANO V., CARRER N.M.,
A GHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
R ENTIAN K.D., ERRINGTON J., FERRARI E., FOULGER D.,
R GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENNOT A.,
HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
A KUBITA K., LAPIDUS A., LARDINOSTEIN G., KROGH S., KUMANO M.,
KUBARASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
KUBITA K., LEPIDUS A., LARDINOSTE S., LAUBER J., LAZAREVIC V.,
B. MEDINA N., MELLADO R., P., MILUO M., MOESTL D., NARAI S., NOBACK M.,
PARRO V., POHL T.M., PORTETLE B., RARPORDILK S., PRESCAT A.M.,
PRESCAN E., PUJIC P., PURTELLE B., RARPOROLIK S., REVNOLDS S.,
R RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
                                                                                                                                                                                                                                                                                                                             325
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                                                                                                                                                                                                                                    QMASIVALEGLVDKEIETMRQAFERRC-DL--AHAKI--NAI-GG--LN-ALKPDGAFYL
                                                                                                                                                                                                                                                                                                                                                               326 FIHIG-SLCGG--DSMRFCHELLEKEGVALVPGKAFGLEGYVRLSFACSEEQIEKGIERI
                                                                                                                          211 -ESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPF
                                                                                                                                                                                              VSCAAVSEEMKKRTITISGLSKSVAMTGWRMGYAASKDKKLVKLMNNLQSQCTSNINSIT
                                                                KDALSPK-TKMLILTTPSNPTGMLYSKAELEVLGEVLKDTKVWVLSDEIYEKLVY-KGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
OUDEGA B., KONINGSTEYN G.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL 39.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-214 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE; 98044033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 ARF 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
DANCHIN A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OUDEGA B.
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SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
SEKIGUCHI J., SEKONSKA A., SEROR S.J., SEROR P., SHIN B.S., SOLDO B.
SOROKIN A., TACCONI E., TARAGI T., TAKAHASHI H., TAKEMARU K.,
TAKENCHI M., TAMAKOSHI A., TAMAKA T., TERPETRA P., TOGNONI A.,
TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
VIARI A., WAMBUTI R., WEDLER E., WEDLER H., WEITZENBGGR T.,
WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
TOSHIKAWA H.F., ZUNSTEIN E., YOSHIKAWA H., DANCHIN A.;
SUDLILIS.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 PDFVTAWNVREASILSLEQG-YTSYTANAGLYSLREEISRYLSNRFDLSYS-PDNELIVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
KATARAMA M., SAKAI Y., OKAMOTO S., IHARA F., NIHIRA T., YAMADA Y.;
KGENE ORGANIZATION in the ada-rpli region of the Streptomyces
virginiae chromosome.";
SUBMITTED (MAX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-! COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-! COFACTOR: PYRIDOXAL PHOSPHATE DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::||::| : :| : :|| : :|| |: |:| |: |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 DFEAAVTEKTKAILICSPSNPTGSVYSKEELNEIAEFAKKHDVIVLADEIYAELTYDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; STREPTOMYCES STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I SIMILAGATA.

MINOTRANSFERAGES.

EMBL, 293934; E311527; -.

EMBL; 299120; E1184218; -.

PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.

PPRA, FF00155; aminotran_1; 1.

HYPOTHETICAL PROTEIN; PYRIDOXAL PHOSPHATE.

247 AA: 39461 MW; FD6B02F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.20e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 FIPMGVF-GHIAPVLSIGSLSKSWIVPGWRLGWVA 302
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PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
PRAM; PF001155; aminotran_1; 1.
TRANSFERSE; PYRIDOXAL E
SEQUENCE 397 AA; 42381 WW; 9240ED06 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
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01-NOV-1996 (TREMBLREL. 01, LAST SEQ0
01-JAN-1999 (TREMBLREL. 09, LAST ANNO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Conservative
                                                                                                                                                                                                                                                                                                                                                           NATURE 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-168;
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Q60013;
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                                                                                                                   81 RDSGYEVEASQVLVTNGGKQAIXEAFAAIL-D-PGDEVIVPAPYWTTYPESIRLAG-GVP 137 : | : | : | : | | : | : | : | | : | |
                                                                                                                                                                               138 -VDVVADETTGYRVSVEQLEAARTERTKVVLFVSPSNPTGSVYSEADAKAIGEWAAEHGL 196
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                                                        25 AAGRPVIGFGAGEPD-FPT-PDYI-VEAAVEAC-RNPKYHRYTPAGGLPELKAAIAAKTL 80
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLE S.T.; "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                            1:: : |: : |: : | : | | : | | 310 LENTRISTSITUYL-NVSTDPA-TFVQEALPRILENTRADFFRRIGLLKESSEI 362
                                                                                                                                                                                                                                                                                                     256 KAAINLQSHAISNVSNVAQVAALAAVSGNLDAVAEMRKA-FDRRRQIMVKMLNEI 309
Score 365; DB 2; Length 397;
Pred. No. 2.14e-48;
76; Mismatches 118; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ئ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.2%; Score 361; DB 2; Length 397; 30.9%; Pred. No. 1.41e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BARRELL B.G., RAJANDREAM M.A. EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; AL022004; E1254000; -.
TRANSFERASE; AMINOTRANSFERASE.
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Query Match 11.3%;
Best Local Similarity 28.5%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TREMBLREL, 06
01-JUN-1998 (TREMBLREL, 06
01-NOV-1998 (TREMBLREL, 08
PUTATIVE AMINOTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37RV;
COLE S.T., PARKHILL J.,
SUBMITTED (FEB-1997) TO
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MEDLINE; 96181548.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 VLSATELAAIAEIAVAANLVVITDEVYEHLVFDHARHLPLAGFDGMAERTITISSAAKMF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 HTH-YADQRGLRELRAALAARLPERPGGAWDADDVLVTHGATAALAAVV-LATVGPGDRV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 VVPEPAYSLYADLVVLAGGTVDFVPLAPDLHW--DLDALAAALP-GAAMMIFSNPSNPTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 IVHRREELEALGKLLDGTDVLVVSDEAYHRLAYPGHEPVSALEIESLRGRTVYVQTFSKT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 YAMIGWRVGYLI--GPREVLDAAAQVHRTWNGSLNTAVQHAALAALDLFDGVVGAMADRY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mb. MICROBIOL. 21:77-96(1996).

EMBL; ALO31411; E1245740; --
TRANSFERASE; AMINOTRANSFERASE.

SEQUENCE 382 AA; 40860 MW; 9FC8F75A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MIATPPASRIAELRRRSRRPALAPAPPGAVSLAMGEPD-FPTPPTVVQA--AVSA-LREG
                                                                                                                                                                                                                                                      STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 LLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSLESIADKNTTAMVIINPNNPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE; 97000351.
REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KINASHI H., HOPWOOD D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 342; DB 2; Length 382;
Pred. No. 1.03e-43;
83; Mismatches 131; Indels 13;
                                                                                                                                                                                                                                                                                                                              STRAIN-A3(2);
MURPHY L., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                            PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                             292 IVPGWRLGWVAVIDPTKILEKTKISTSITNYLNVST-DPA 330
                                                          235 NCTGWKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA
                                                                                                                                                  382 AA
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06,
08,
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Best Local Similarity 26.1%;
Matches 80; Conservative
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01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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RESULT

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TRAINCHINE: 98144137.

RA MARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,

RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,

RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,

FUNDHARBHI T., TANNKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,

RA AOKI K., NAKAWURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,

RA KIKUCHI H.;

RY "Complete Sequence and Gene Organization of the Genome of a

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RY "TANSFERASE: AMINOTRANSFERASE.

KW TRANSFERASE: AMINOTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AYEGTYLAFESLLER-GDEVIIPDPAFVSYAEDAKVAEAK-PVR-IPLREENNFLPDPNE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 LLEKIS-KNTR-MIVINYPNNPTGATLD-KELAKTIADIAEDYNIYILSDEPYEHFIYED 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 - NVASFVQIAGIEAL-RS-EESWKAVEEMKKEYNERRKIVVKRLKNMPGIKVKEPKGAFY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 TDPATFVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCPH-K-PEGSMF 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 VFPNIS-G--TGMSSE-KFSEWLLEKARVVVIPGTAFGRMGEGYVRISYATSKEKLIEAM 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 VMVKLNLHLLEEIHDDIDFCCKLAKEESVILCPGSVLG-M-ENWVRITFACVPSSLQDGL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                             ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 AKHYPMIKFAPENTILA-NSFSKTFAMTGWRLGFV-V-APSQVI-K-EM-TKLHAYV-IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.2%; Score 330; DB 1; Length 391; Best Local Similarity 28.4%; Pred. No. 2.75e-41; Matches 103; Conservative 82; Mismatches 148; Indels 30;
                                          01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
391AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
391 AA.
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ne : 39 secs.
  PRT;
  PRELIMINARY;
                                                                                                                                                          PYROCOCCUS HORIKOSHII
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Oct 1 13:51:53 1999; MasPar time 22.78 Seconds 810.770 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-026-400-2 (1-461) from USO9026400.pep 3223 1 MVHQSNGHGERAAAAANGKS.....LERVKSFCQRNKKNSINGC 461 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 49.862; Variance 105.736; scale 0.472 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		оP			SUMMAKIES		
Result No.	Score	Query	Query Match Length DB	DB	ΩI	Description	Pred. No.
П	920	28.5	454	-	XNRTY	tyrosine transaminasa	2 110-146
8	914	28.4	454	7	510887		3 080-140
Э	495	15.4	4	8	H70506	-	
4	439		401	7	D71003		4.22P-55
w	410	12.7	405	7	H65000	hypothetical protein	
Q	403	12.5	394	7	A70469	aspartate aminotransf	1.476-48
7	394	12.2	402	ď	80708		6.17e-47
∞	376	11.7		~	H71909		1.05e-43
0	374	11.6		N	H64603	hypothetical protein	2.40e-43
10	368	11.4		~	G70010	aspartate aminotransf	2.836-42
11	368	11.4		N	A64300	aspartate transaminas	2.83e-42
12	361	11.2	397	~	B70815	hypothetical protein	5.00e-41
13	358	11.1	392	7	A38621	aspartate transaminas	1.71e-40
14	330	10.2		7	E71125	probable aspartate am	1.50e-35
15	330	10.2		~	C69591	aspartate aminotransf	
16	323	10.0		7	A69516		2.52e-34
17	308	9.6	412	7	B71718		1.03e-31
18	299	9.3	389	7	E71009		3.69e-30
13	299	ω.	392	7	C69672		3.69e-30
20	300	œ.	592	7	S64923	membrane p	2.48e-30
21	296	9.5	383	7	JC5775	aspartate transaminas	1.21e-29
22	295	9.5	382	7	JC4537	aspartate transaminas	80e-2
23	294	9.1	374	7	G69119	aspartate aminotransf	68e-2

9.1 507 2 \$52677 probable membrane pro 2 68e-29 8.8 400 2 \$447094 aspartate transaminas 9 .38e-28 8.6 373 2 \$E70338 aminotransferase (Asp 2.15e-26 8.3 2 \$73.4 4	NNRT Foro 0-Sz 2233 2233 2233 726 8 ne	11804 YPE MRNA 266-284, Tences GB:MI the auth Pro part of sequen N0343 Sequen Sequen Sequen Corg. Khim. Icleotide se aminotransf aminotransf aminotransf seguen Sequen Seq
24 25 26 27 27 29 29 29 20 30 30 31 31 32 33 33 34 36 36 37 37 37 37 38 39 39 20 40 41 41 41 42 41 42 41 44 41 41 41 41 41 41 41 41 41 41 41	9 O O O O	accession ##molecule ##molecule ##roiss-ref ##note ##note ##note authors journal title title cross-referen accession ##molecule
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#journal Eur. J. Biochem. (1991) 201:399-407
#title Expression of mammalian tyrosine aminotransferase in Saccharomyces cerevisiae and Escherichia coli. Purification to homogeneity and characterization of the enzyme overproduced in the bacteria.
#cross-references MUID:92037592
                                                                                                                                                                                                                                                                                                                                                                                       Isolation and characterization of active N-terminal truncated apo- and holoenzyme of mammalian liver tyrosine aminotransferase.
                                                                                                                Nucleotide sequence of rat liver tyrosine aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 SNKTFNPIRAIVDNMKVQPNPNKTVISLSIGDPTVFGNLPTDPEVTQAMKDALDSGKYNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 YAPSIGYLSSREEVASYYHCHEAP--LEAKDVILTSGCSQAIELCLAVLAN-PGQNILIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 RPGFSLYRTLAESMGIEVKLYNLLPEKSWEIDLKQLESLIDEKTACLVVNNPSNPCGSVF 225
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#binding_site pyridoxal phosphate (Lys) (covalent)
#status experimental
#length 454  #molecular-weight 50635  #checksum 7044
                                   A48430
Morozov, I.V.; Mishin, V.P.; Zelenin, S.M.; Popova, V.S.
Metrvetsov, N.P.
DNA Seq. (1990) 1:151-155
                                                                                                                                                                                                                                                                                         sequence extracted from NCBI backbone (NCBIN:89708 NCBIP:89709)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #modified_site acetylated amino end (Met) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.5%; Score 920; DB 1; Length 454; Best Local Similarity 34.3%; Pred. No. 2.11e-146; Matches 137; Conservative 117; Mismatches 135; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *superfamily mammalian tyrosine aminotransferase acetylated amino end; aminotransferase; homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not compared with conceptual translation
                                                                                                                                                                                                                    ##molecule_type DNA
##cresidues 190-284,'L',286-386 ##label MOR
##cross-references GB:X15690; NID:957845; PID:91334238
##experimental_source_liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprotein; pyridoxal phosphate
                                                                                                                                                                                                                                                                                                                                                         Lorber, B.; Dietrich, J.B.; Kern, D. FEBS Lett. (1991) 291:345-349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##experimental_source liver NCE 517849 ....cs 517849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1,'V',3-10 ##label DIE ##experimental_source liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #region PEST sequence\
385-454 ##label ZEL
                                                                                                                                 gene fragment.
#cross-references MUID:92190544
#accession A48430
                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:92038067
#accession S18308
                                                                                                                                                                                               preliminary
              ##experimental_source liver
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##molecule_type protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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##residues
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##cross-references GDB:120398; OMIM:276600
#map_position 16q22.1-16q22.3
#introns 79/1; 114/1; 136/3; 189/3; 236/1; 253/3; 304/3; 347/3; 375/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *authors Seralini, G.E.; Breton, N.; Berube, D.; Gagne, R.; Labrie, F *submission submitted to the EMBL Data Library, September 1990 *description Nucleotide sequence of human tyrosine aminotransferase CDNA. *accession $21425
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##residues 1-454 ##label RET
##cross-references EMBL:X52509; NID:g36696; PID:e225804; PID:g1217965
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Biochim. Biophys. Acta (1995) 1260:97-101
Cloning and expression of human tyrosine aminotransferase
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                                                295 GWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKADFFKRIIG 354
                                                                                                     345 FLKSNADLCYGALAAIPGLQ-PVRPSGAMYLMVGIEMEHFPEFENDVEFTERLIAEQAV- 402
                                                                                                                                  355 LLKESSEICYREIKENKYITCPHKPEGSMFVWVKLNLHLLEEIHDDIDFCCKLAKEESVI 414
286 GWRLGWILIHDRRDIFGN-EIRDGLVKLSQRILGPCTIVQGALKSILQRTPQEFYHDTLS 344
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04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
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##residues 1-454 ##label SER
##cross-references EMBL:X55675; NID:g37501; PID:g37502
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Bioorg. Khim. (1994) 20:196-204
Nucleotide sequence of human tyrosine
S60718
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#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
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##cross-references GB:297991; GB:AL123456; NID:93261837; PID:e330321;
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Pred. No. 2.11e-65;
86; Mismatches 155; Indels 15; Gaps
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
109 YAPSIGFLSSREEIASYY-HCPEAPLEAKDVILTSGCSQAIDLCLAVLAN-PGQNILVPR
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##residues 1-401 ##label KAW
##cross-references GB:AP000006; NID:g3236133; PID:d1031371; PID:g3257745
##experimental_source strain 0T3
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GLPAARSAVAEH-LSQGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILLPRPGYP 179
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                                                                                                                             LWTASTSLAGGTPVHY - LCDETQGWQPDIADLESKITER-TKALVVINPNNPTGAVYSCE
                                                                                                                                                                                               this accession replaces an interim accession for sequence replaced by GenBank
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Pred. No. 4.22e-55;
83; Mismatches 135; Indels 13;
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:AD000318; GB:U00096; NID:g1788623; PID:g1788627; ##cross-references GB:AD000318; GB:U00096; NID:g1788627;
                                                                                                                                                                                                   - Escherichia coli (strain K-12)
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LAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVEGHIAPVLSIGSLSKSWIVPGWRL 298
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 17 IRGPVLKEAKRLEEEGNK-VLKLNIGNPAPF-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
                                                                                                                                                                       hypothetical protein b2290 - Escherichia coli (strain K-hypothetical protein b2290 - Escherichia coli 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 14-Nov-1997
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                                                                                                                                                                                                                                                                                                                                                      #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references_MUID:97426617
                                            SEVREAIDKLARIRICPNTPGQFA--AIAG-LTGSM-DYLKEYMKKLKERRDFIYKRLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 410; DB 2; Length 405;
larity 27.3%; Pred. No. 7.94e-50;
Conservative 94; Mismatches 154; Indels 18;
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Y #length_405 #molecular-weight_45517 #c
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                                                                                                      318 IPGIS-TTKPQGAFYIFPRIE 337
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Best Local Similarity
Matches 100; Conserv
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Cubells, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino, G.; Sannia, G.
G.; Sannia, G.
Bur. J. Biochem. (1989) 186:375-381
Cloning and sequencing of the gene coding for aspartate
aminotransferase from the thermoacidophilic archaebacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-394 ##label AQF ##cross-references GB:AE000766; NID:g2984216; PID:g2984217; GB:AE000657 ##experimental_source strain VF5
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                                                                                                                                                    Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
                           #formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
                                                                                                                                                                                                                                                                          #title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
#cross-references MUID:98196666
#accession A70469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 PDFDTPDFIKEACIRALREGKTK-YAPSAGIPELREAIAEKLLKENKVEYK-PSEIV-VS
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#superfamily aspartate transaminase
#length 394 #molecular-weight 43777 #checksum 8792
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Pred. No. 1.47e-48;
87; Mismatches 145; Indels
- Aquifex aeolicus
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translation not shown
     aminotransferase
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$07088
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Best Local Similarity 29.1%;
Matches 106; Conservative
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#formal_name Helicobacter pylori
strain J99
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                                                                                                                                                                              G.; Pucci,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 MYDELTKVKGVEVS-KPNGAFYMFPNVSKILKTSGFDVKSLAIKLIEEKGVVTIPGEVFP
                                                                                                                                                                                                                                                                                                                                                                                   #Superfamily aspartate transaminase
aminotransferase
#length 402 #molecular-weight 45732 #checksum 791
                                                                                                                                                                                                                          #fitle Post-translational modifications in aspartate aninotransferase from Sulfolobus solfataricus.
Nepsilon-methyllysines by mass spectrometry.
#cross-references MUID:94298815
                                                                                                                                                                Zappacosta, F.; Sannia, G.; Savoy, L.A.; Marino,
P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 394; DB 2; Length 402;
Pred. No. 6.17e-47;
                                                                                                                         ##molecule_type protein
##residues 2-38;297-306;308-327;400-402 ##label CU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 118; Mismatches 153; Indels
                                                                           ##residues _ 1-402 ##label CUB
##cross-references EMBL:X16505; NID:g47497; PID:g809765
                                                                                                                                                                                                            Eur. J. Biochem. (1994) 222:761-767
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Sulfolobus solfataricus.
#cross-references MUID:90092126
#accession S07089
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24.7%;
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Matches 96; Conserv
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Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.Y.; Bergy, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujil, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                          GB:AE001439; NID:94155161; PID:94155168
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Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.
#journal Nature (1999) 397:176-180
#fitle Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter Pylori.
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hypothetical protein HP0672 - Helicobacter pylori (strain
26695)
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30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change
13-Sep-1998
H64603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 DPATEVQ-EAL-PRILENTKADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 KDALSPK-TKMLILTTPSNPTGMLYSKAELEALGEVLKDTKVWVLSDELYEKLVY-KGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily aspartate transaminase
#length 390 #molecular-weight 42746 #checksum 4845
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Pred. No. 1.05e-43;
83; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                     ##residues 1-390 ##label ARN
##cross-references GB:AE001493; GE
##experimental_source strain J99
                                                                                                                                                                                                               ##molecule_type DNA
##residue
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Best Local Similarity 27.3%;
Matches 99; Conservative
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AKQSLFNAIQALIE-EGDEVIIPVPFWVTYPELVKYSG-GVSQFIQTDEKSHFKITPKQL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 PDFDTPQAIKDAAIKALNDG-FTKYTPVAGIPELLKAIAFKLKKENNLDYEPNEILVSNG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 VSCAAVSEEMKKRTITISGLSKSVAMTGWRMGYAASKDKKLVKLMNNLQSQCTSNINSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 KDALSPK-TKMLILTTPSNPTGMLYSKAELEVLGEVLKDTKVWVLSDEIYEKLVY-KGEF
                                                                                                                                                                                                          ##residues 1390 ##label TOM ##residues 1390 ##label TOM ##cross.references GB:AE000511; TIGR:HP0672 CLASSIFICATION #superfamily aspartate transaminase sumMARY #length 390 #molecular-weight 42874 #checksum 4436
                                                                              preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 374; DB 2; Length 390;
Pred. No. 2.40e-43;
85; Mismatches 158; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 390;
                                                                                                                                translation not shown
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#cross-references MUID:97394467
#accession H64603
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Local Similarity 26.7%;
les 97; Conservative
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                                                                                                                                                                               ##molecule_type DNA
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Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, Bult, C.J.; White, O.; Olsen, G.J.; EtrzGerald, L.M.; Clayton, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Xirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klerk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073 Complete genome sequence of the methanogenic archaeon,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, T.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Scklquchi, J.; Sckowska, A.; Serror, R.; Scroffone, F.; Scklquchi, J.; Sckowska, A.; Serror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wedler, E.; Wedler, H.; Weltzenegger, T.; Winter, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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13-Sep-1996_#sequence_revision 13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 AGGTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNK-LEVRHFDLIPDKGWEIDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 DFEAAVTEKTKAILICSPSNPTGSVYSKEELNEIAEFAKKHDVIVLADEIYAELTYDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily aspartate transaminase
#length 357 #molecular-weight 39461 #checksum 3672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 368; DB 2; Length 357; Pred. No. 2.83e-42;
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Best Local Similarity 29.8%;
Matches 64; Conservative
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PID:g2916917
                                                                                                                                                                 ##cross-references GB:U67459; GB:L77117; NID:g1590815; PID:g1592252; ##cross-references GB:U67459; GB:L77117; NID:g1590815; PID:g159252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ASEALMLSIMTLIDR-GDEVLIPNPSFVSYFSLTEFAEGKIKNIDL--DENFNIDLEKVK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSL- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B70815 #type complete
hypothetical protein Rv0858c - Mycobacterium tuberculosis
(strain H37RV)
#formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 PAFRIAVEAEDAVAAALRIGGFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLIAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 PDFDTPKHIIEAAKRALDEGKTH-YSPNNGIPELREEISNKLKDDYNLDVDKDNIIVTCG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIFAQYGALA-ALRGSQ-KCVEDMVREFKMRRDLIYNGLKDI-FKV--NKPDGAFYI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 ESIT-KKTKLIIFNSPSNPTGKVYDKETIKGLAEIAEDYNLIIVSDEVYDKIIYDKKHYS
                                                                                                                                                                                                                                                                                                                                                                                       #checksum 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 368; DB 2; Length 375;
Pred. No. 2.83e-42;
84; Mismatches 117; Indels 18;
                                                                                           sequence not shown;
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                                                                                                                                                                                                                                                                                                                       #superfamily aspartate transaminase
aminotransferase
#length 375 #molecular-weight 42395
                                                                                        nucleic acid
                                                                                  preliminary; nucleic actrianslation not shown
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Methanococcus jannaschli.
#cross-references MUID:96337999
#accession A64300
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.4%;
Best Local Similarity 26.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                        #map_position REV3343-2216
CLASSIFICATION #superfamily
                                                                                                                                            ##molecule_type DNA
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A70500
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                                                                                     ##status
                                                   #accession
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#journal J. Biol. Chem. (1991) 266:2567-2572
#title Thermostable asparted aminotransferase from a thermophilic
Bacillus species. Gene cloning, sequence determination, and
#cross-references WID:91115885
#accession A38621
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                                                                                                                                                                                                                                                                             57 YPPGPGSAPLRRAIAAQRRRHFGVDYD-PETEVLVTVGATEAIAAAVLGLVE-PGSEVLL 114
                                                                                                                                                                           115 IEPFYDSYSPVVAMAGAHRVTVPLVPDGRGFALDADALRRAVTPRTRALIINSPHNPTGA 174
                                                                                                                                                                                                                                                                                                                                               175 VLSATELAAIAEIAVAANLVVITDEVYEHLVFDHARHLPLAGFDGMAERTITISSAAKMF 234
                                                                                                                                                                                                                                                                                                                                                                            233 VYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIA-PVLSIGSLSKSW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 PDFNTPQNIMDAAIDSMQQG-YTKYTPSGGLPALKQAIIEKFKRDNQLEYKPNEIIVGVG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 KNAITDK-TKAVIINSPSNPTGMVYTREELEDIAKIALENNILIVSDEIYEKLLYNGAEH 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSIAQISEEVKAQTIVINGVSKSHSMTGWRIGYAAG-NADIINAMTDLASHSTSNPTTAS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |: : | | : ::: : | : : | | : | | : | DPATFVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVWV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Bacillus sp.
23-Aug-1991 #text_change
13-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AKHVLYTLFQVILN-EGDEVIIPIPYWVSYPEQVKLAG-GVPVYIEATSEQNYKITAEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 FIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sung, M.H.; Tanizawa, K.; Tanaka, H.; Kuramitsu, S.;
Kagamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi,
#length 397 #molecular-weight 42209 #checksum 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #checksum 7039
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11.1%; Score 358; DB 2; Length 392;
Best Local Similarity 23.5%; Pred. No. 1.71e-40;
Matches 85; Conservative 105; Mismatches 154; Indels 18;
                                                    Length 397;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references GB:M59430; NID:g142537; PID:g142538 CLASSIFICATION #superfamily aspartate transaminase AEYWORDS aminotransferase
                                               Score 361; DB 2; Le
Pred. No. 5.00e-41;
56; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 NCTGWKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 IVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST-DPA 330
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                                               h
Similarity 30.9%;
68; Conservative
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                                               Query Match
Best Local Similarity
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REFERENCE
#authors
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   443
                                                                                                                                                              TITLE
ORGANISM
DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosuqi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogusa, R.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Offuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                 probable aspartate aminotransferase - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mplete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFPNIS-G--TGMSSE-KFSEWLLEKARVVVIPGTAFGRMGEGYVRISYATSKEKLIEAM 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAFRIAVEAEDAVAAALRIGOFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLIAG 151
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                                     329 DVSEAAQKTGFASVDEFASALLTEANVAVIPGSGFGAPSTIRISYATSLNLIEEAIERID
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Pred. No. 1.50e-35;
82; Mismatches 148; Indels 30;
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Best Local Similarity 28.4%;
Matches 103; Conservative
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##residues 1-393 ##label KUN
##cross-references GB:299115; GB:AL009126; NID:g2634478; PID:e1183682;
##Cross-references PID:g2634655
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                                                                                 #formal_name Bacillus subtilis
05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily aspartate transaminase
#length 393 #molecular-weight 43088 #checksum 6856
                               aspartate aminotransferase aspB - Bacillus subtilis
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Pred. No. 1.50e-35;
117; Mismatches 145; Indels 20;
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#type complete
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Local Similarity 23.2%;
nes 85; Conservative 1
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Oct 1 13:50:18 1999; MasPar time 15.42 Seconds 844.953 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-09-026-400-2 (1-461) from USO9026400.pep 3223 1 MYHQSNGHGEAAAAANGKS......LERVKSFCQRNKKKNSINGC 461 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 51.018; Variance 91.346; scale 0.559 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	3 490-173	8 326-172	5.46e-94	1.09e-55	3.41e-50	4.28e-48	2.22e-45	2.86e-42	2.51e-36		6.58e-35	4.29e-33	1.01e-27	3.91e-27	2.09e-24	8.56e-25	3.00e-23	1.75e-22	9.06e-21	1.40e-20	9.06e-21	7.96e-20	1.06e-18
	Description	TYROSINE AMINOTRANSEER			ASPARTATE AMINOTRANSFE	PUTATIVE ASPARTATE AMI	ASPARTATE AMINOTRANSFE	ASPARTATE AMINOTRANSFE	ASPARTATE AMINOTRANSFE	PUTATIVE AMINOTRANSFER	PUTATIVE ALANINE AMINO	PUTATIVE ALANINE AMINO	ASPARTATE AMINOTRANSFE	HYPOTHETICAL AMINOTRAN	PUTATIVE ALANINE AMINO	ASPARTATE AMINOTRANSFE	HYPOTHETICAL AMINOTRAN	HYPOTHETICAL AMINOTRAN	ALANINE AMINOTRANSFERA	PUTATIVE AMINOTRANSFER	PROBABLE ASPARTATE AMI	1-AMINOCYCLOPROPANE-1-	ALANINE AMINOTRANSFERA	PROBABLE ASPARTATE AMI
	Ü	ATTY_RAT	ATTY HUMAN	ATTY_TRYCR	AAT_SULSO	AAT1_METJA	AAT_BACSP	AAT_BACST	AAT1_BACSU	PATA_BACSU	ALAM_YEAST	ALAT_YEAST	AATA_RHIME	YJGO_YEAST	ALAT_SCHPO	AATB_RHIME	YDT4_SCHPO	YBDL_ECOLI	ALA2_HORVU	PATB_BACSU	AAT2_BACSU	1A1C_DIACA	ALA2_PANMI	AAT_STRGR
	DB	: -	Н	Н	Н	П	Н	П	Н	Н	, 1	Н	Н	Н	П	Н	H	m	,	Н	Н	Н	ч	Н
	Length	454	454	416	401	375	392	393	393	392	592	202	400	444	202	410	421	386	482	387	399	517		213
dР	Query	28.5	28.4	17.7	12.2	11.4	11.1	10.7	10.2	6. م	9.3		æ. æ	8.0	7.9	7.5	٠	7.3	•	6.9	٠	6.9	6.7	6.5
	Score	920	914	570	394	368	358	345	330	301	300	294	285	258	255	241	243	235	231	222	221	222	217	211
	Result No.	н	2	m	4	ហ	ا م	7	ж ·	on ;	10	11	12	13	14	15	97	17	87	19	20	21	22	23

1 060-18	٠ <u>-</u>	H	1.756-16	9.446-16	9.446-16	2.64e-14			1.586-12	2.37e-12	2.64e-11		1.92e-10	2.85e-10		1.36e-09	_		6e-0	426-0	.41e-	
HISTIDINOL-PHOSPHATE A	ы	HYPOTHETICAL AMINOTRAN	1-AMINOCYCLOPROPANE-1-	HISTIDINOL-PHOSPHATE A	~~	HYPOTHETICAL 53.0 KD P		1-AMINOCYCLOPROPANE-1-	1-AMINOCYCLOPROPANE-1-	ᆸ	MALY PROTEIN (EC 2.6.1	1-AMINOCYCLOPROPANE-1-	PUTATIVE ASPARTATE AMI	1-AMINOCYCLOPROPANE-1-	1-AMINOCYCLOPROPANE-1-	HISTIDINOL-PHOSPHATE A		- 63	PROBABLE AMINOTRANSFER	HISTIDINOL-PHOSPHATE A	ρ	
HIS8 YEAST		YFDZ_ECOLI	1A12_CUCMA	HIS8_HALVO	ALAT_RAT	YJIR_ECOLI	HIS8_SULSO	1A11_CUCMA	1A11_CUCPE	ALAT_HUMAN	MALY_ECOLI	1A12_CUCPE	AAT2_METJA	1A1C_MALDO	1A14_LYCES	HIS8_MYCSM	HIS8 SCHPO	YU16 MYCTU	YB66_HAEIN	HIS8_SALTY	HIS8_METJA	
7	П	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	_	Н	-1	Н	Н	7	Н	
385	418	412	475	361	495	470	376	493	493	495	390	464	370	473	476	219	384	407	366	359	373	
6.5	6.5	6.4		6.1		5.8	•		5.5				5.1						4.9		4.8	
211	210	207	199	195	195	187	185	179	177	176	170	166	165	164	163	160	162	160	158	155	156	
24	22	56	27	78	53	30	31	32	33	34	35	36	37	38	90	40	41	42		44	45	

ALIGNMENTS

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HOMO
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                                                                                                                                                                                                                                                                                                                                                                                       pred. No. 3.49e-173;
117; Mismatches 135; Indels 11; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWRLGWILIHDRRDIFGN-EIRDGLVKLSQRILGPCTIVQGALKSILQRTPQEFYHDTLS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 LLKESSEICYREIKENKYITCPHKPEGSMFVMVKLNLHLLEEIHDDIDFCCKLAKEESVI 414
                                                                                                                                                                                                                                                                                                                                                                                                                    49 SNKTFNPIRAIVDNMKVQPNPNKTVISLSIGDPTVFGNLPIDPEVTQAMKDALDSGKYNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AKNSIRAIRYKISA-SVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQFNC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAPSIGYLSSREEVASYYHCHEAP -- LEAKDVILTSGCSQAIELCLAVLAN-PGQNILIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKRHLQKILAVAERQCVPILADEIYGDMVFSDCKYEPLANLSTNVPILSCGGLAKRWLVP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 FLKSNADLCYGALAAIPGLQ-PVRPSGAMYLMVGIEMEHFPEFENDVEFTERLIAEQAV- 402
                                              -:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- PATHWAY: FIRST STEP IN THE CATABOLISM OF TYROSINE.
-:- SUBUNIT: HOMODIMER.
-:- TISSUE SPECIFICITY: LIVER.
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                 PFAM; PF00155; aminotran_1; 1.
TYROSINE CATABOLISM; TRANSFERASE; AMINOTRANSFERASE; ACETYLATION;
 and immunochemical properties of rat liver tyrosine
                                                                                                                                                                                                                                                                                                                                                                              Length 454;
                                                                                                                                                                                                                                                                                     PYRIDOXAL PHOSPHATE.
IV -> KT (IN REF. 2).
TA -> LE (IN REF. 3).
MISSING (IN REF. 3).
AI -> DL (IN REF. 3).
A -> DL (IN REF. 2).
A -> DL (IN REF. 2).
A -> D (IN REF. 2).
                               2-OXOGLUTARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCLPATCFEYPNFFRVVIT-VPEVMMLEACSRIQEFCEQH 441
                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                  BIOCHIMIE 70:673-679(1988).
-!- CATALYTIC ACTIVITY: L-TYROSINE + 2-OXC 4-HYDROXYPHENYLPYRUVATE + L-GLUTAMATE.
                                                                                                                                                                                                                                        PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                               ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                               Score 920;
                                                                                                                                                                                                                                                                                                                                                            50635 MW;
                                                                                                                                                                                                                                                                                                                                                                                28.5%;
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.3%;
Matches 137; Conservative
                                                                                                                                                                                                EMBL; X02741; G57328; -. EMBL; M18340; G207156; -. EMBL; X15690; G57846; -.
                                                                                                                                                                                                                                                                                       280
210
210
385
360
445
                                                                                                  AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                        280
59
209
285
304
359
445
454 AA;
                                                                                                                                                                                                                                                                     PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                              PIR; A23310; XNRTY.
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CONFLICT
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CONFLICT
SEQUENCE
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454 AA

PRT;

STANDARD;

T 2 ATTY_HUMAN

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE, 93028451.
MATT E., KIDA K., ODIEVRE M., DI ROCCO M., SCHERER G.;
"Point mutations in the tyrosine aminotransferase gene in tyrosinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- CATALTIC ACTIVITY: L-TYGSINE + 2-OXOGLUTARATE = 4-HYDROXYPHENYLPYRQYEE + 1-CLUTAWATE.
-:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- PATHWAT: FIRST STEP IN THE CATABOLISM OF TYROSINE.
-:- PATHWAT: ROMODIMER.
-:- SUBUNIT: HOMODIMER.
-:- TISSUE SPECIFICITY: LIVER.
-:- DIEBASE: DEFECTS IN TAT ARE THE CAUSE OF TYROSINEMIA TYPE II (RICHNER-HANHART SYNDROME).
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95092801. SERLIN G.E., LABRIE F.; SERALINI G.E., LUUTHE V., LABRIE F.; C.CONING and expression of human tyrosine aminotransferase CDNA."; BIOCHIM. BIOPHYS. ACTA 1260:97-101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSUULUJ; AMINOTRANSFERASE;
TYROGISE; AMINOTRANSFERASE;
TYROGINE CATABOLISM; TRANSFERASE; AMINOTRANSFERASE;
PYRIDONAL PHOSPHATE; DISEASE MUTATION.
BINDING 280 280 PYRIDONAL PHOSPHATE (BY SIMILARITY).
362 362 G -> V (IN TYROSINEMIA, TYPE II).
VARIANT 362 362 WW; 2030555D CRC32;
01-AUG-1990 (REL. 15, CREATED)
1-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST AND TATION UPDATE)
TYROSINE AMINOFRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE
                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAB; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE; 90326506.
RETTENMEIER R., NATT E., ZENTGRAF H., SCHERER G.;
"Isolation and characterization of the human tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type II.";
PROC. NATL. ACAD. SCI. U.S.A. 89:9297-9301(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aminotransferase gene.";
NUCLEIC ACIDS RES. 18:3853-3861(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X52509; E225804; --
EMBL, X52510; E225804; JOINED.
EMBL, X52511; E22804; JOINED.
EMBL, X52513; E22804; JOINED.
EMBL, X52513; E22804; JOINED.
EMBL, X52513; E22804; JOINED.
EMBL, X52514; E22804; JOINED.
EMBL, X52515; E22804; JOINED.
EMBL, X52516; E22804; JOINED.
EMBL, X52516; E22804; JOINED.
EMBL, X52518; E22804; JOINED.
EMBL, X52519; E22804; JOINED.
EMBL, X52519; E22804; JOINED.
EMBL, X5250; G36713; --
EMBL, X55575; G3573; --
PIR, X10887; S10887.
                                                                                                                                                       AMINOTRANSFERASE) (TAT).
                                                                                                                                                                                                                          SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90326506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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6
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                                                                                    57 AKNSIRAIRYKISA-SVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRIGQFNC 115
                                                                                                                  YAPSIGFLSSREEIASYY-HCPEAPLEAKDVILTSGCSQAIDLCLAVLAN-PGQNILVPR 166
                                                                                                                                                                                                                                                              LKSNADLCYGALAAIPGLR-PVRPSGAMYLMVGIEMEHFPEFENDVEFTERLVAEQSV-H 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALTIC ACTIVITY: L-TYROSINE + 2-OXOGLUTARATE =
4-HYDROXYPHENYLPRUVATE + L-GLUTAMATE.
AN AROMATIC OXO ACID + L-GLUTAMATE.
COFACTOR: PYRIDOXAL PHOSPHATE.
PATHWAY: FIRST STEP IN THE CATABOLISM OF TYROSINE.
SUBUNIT: HOWODIMER.
SUBCELLOLAR LOCATION: MAINLY CYTOSOLIC. PRESENT TO A SWALL EXTENT IN THE MITOCHOMBIAL FRACTION.
FIN: THERE DISULFIDE BONDS ARE PRESENT.
PTM: THREE DISULFIDE BONDS ARE PRESENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MONTEMARTINI M., SANTOME J.A., CAZZULO J.J., NOWICKI C.;
"Purification and partial structural and kinetic characterization of
tyrosine aminotransferase from epimastigotes of Trypanosoma cruzi.";
BIOCHEM. J. 292.901-906(1993).
-!- FUNCTION: COULD TRANSAMINATE TRYPTOPHAN, PHENYLALANINE AS WELL
AS TYROSINE. THIS PARTICULAR ENZYME MAY ALSO BE AN ALANINE
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA
                                                                                                                                                                               PGFSLYKTLAESMGIEVKLYNLLPEKSWEIDLKQLEYLIDEKTACLIVNNPSNPCGSVFS
                                                                                                                                                                                                                                        227 KRHLQKILAVAARQCVPILADEIYGDMVFSDCKYEPLATLSTDVPILSCGGLAKRWLVPG
                                                                                                                                                                                                                                                                                                                         WRLGWILIHDRRDIFGN-EIRDGLVKLSQRILGPCTIVQGALKSILCRTPGEFYHNTLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
1 UNOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
TYROSINE AMINOFRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE
AMINOTRANSFERASE) (TATA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 120-148; 153-167 AND 324-338, AND CHARACTERIZATION.
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ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 93341574.
BONTEMPI E.J., BUA J., ASLUND L., PORCEL B., HENRIKSSON J.,
BONTEMPI E.J., BUA J., ASLUND L., PORCEL B., HENRIKSSON J.,
ISOLATION and characterization of a gene from Trypanosoma c
encoding a 46-kilodalton protein with homology to human and
tyrosine aminotransferase.";
   DB 1; Length 454;
                               Indels
 Score 914; DB 1; Le
Pred. No. 8.32e-172;
119; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                              CLPATCFEYPNFIRVVIT-VPEVMMLEACSRIQEFCEQH 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. BIOCHEM. PARASITOL. 59:253-262(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 28, CREATED)
ch 28.4%;
1 Similarity 33.6%;
134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UL 0;
93305080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TUL
MEDLINE; 93
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Query Match
               Local
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                            Matches
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                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUBELLIS M.V., ROZZO C., NITTI G., ARNONE M.I., MARINO G., SANNIA G., "Cloning and sequencing of the gene coding for aspartate aminotransferase from the thermoacidophilic archaebacterium
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                      16
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                   18 PIR-TVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQECNGYFPTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                              PGFPHYETVCKAYG-IGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNPSNPCGSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 SRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 LVVPGWRLGWL-LYVDPHGNGPSFLEGLKRVGML-VC-GPCTVVQAALGEALLNTPQEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 WIVPGWRLGWVAVY-DPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKADFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 DQIVAKIEESAMYLYNHIGECIGLA-PIMPRGAMYLMSRIDLEKYRDIKIDVEFFEKLLE
                                                                                                                                                                                                                                              PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT). SULFOLOBUS SOLFATARICUS.
                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                           Length 416;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 EENVQVL-PGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRH 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 1-38 AND 296-326.
STRAIN-ATCC 49255 / MT4;
                                                                                                                                                                            PROSITE; PS00105; AA TRANSPER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TYROSINE CATABOLISM; TRANSPERASE; AMINOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                      Pred. No. 5.46e-94;
105; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
                                                                                                                                                                                                                                                                                                      17.7%; Score 570; DB 1; 30.9%; Pred. No. 5.46e-94;
                                                                                                                                                                                                                                                           153 H -> D (IN REF. 2
46167 MW; AC035E2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT SULSO STANDARD; PRT; 401 AA. P149091 (REL. 14, CREATED) 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfataricus.";
EUR. J. BIOCHEM. 186:375-381(1989).
                                                                                                                                                                                                                                                                                                                                      Conservative
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SEQUENCE, AND METHYLATION.
                                                                                                                                                                                                                                           253
                                                                                                                                                                EMBL; L00673; G408894;
                                                                                                                                                                                                                                                        153 1
416 AA;
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                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 125; Conser
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Matches
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AAT1_METJA
Q60317:
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                                                                                                                                                                                                                                        421
                                                                                                                                                                                            365
                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIAPVLSIGSLSKSWIVPGWRLGWVA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 VKLLGGKPIYANLKWSREEGFSIDVDDLQSKISKRTKMIVFNNPHNPTGTLFSPNDVKKI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDISRDNKIILLSDEIYDNFVYEGKMRSTLEDSDWRDFLIYVNGFSKTFSMTGWRLGYI- 253
                                       ZAPPACOSTA F., SANNIA G., SAVOY L.-A., MARINO G., PUCCI P.; "Post-translational modifications in aspartate aminotransferase from Sulfolobus solfataricus. Detection of N-epsilon-methyllysines by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 YK-ISASVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 LREKIAQYLNTRYGTDVKKEEVIVTPGAKPALFLVF-ILYINPSDEVILPDPSFYSYAEV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 YKEIARNVEKTKKIKIIDFGIGQPDL-PTFKR-IR--DAAKEALDQG-FTFYTSAFGIDE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBGNIT: HOMODIMER.
-!- THIS ENZIME OPTIMUM TEMPERATURE IS ABOVE 95 DEGREES CELSIUS.
-!- THIS ENZIME OPTIMUM CEMPERATURE IS PYRIDOXAL-PHOSPHATE-DEPENDENT
-!- SIMILARIYE: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                    "Purification and characterization of aspartate aminotransferase the thermoacidophilic archaebacterium Sulfolobus solfataricus."; J. BIOL. CHEM. 263:12305-12309(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S21189; S21189.
PROSITE: PSO0105; AA.TRANSFER_CLASS_1; 1.
PFAM; PFO0155; aminoLiran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE; METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                              o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRIDOXAL PHOSPHATE.
METHYLATION (MONO-) (PARTIAL).
METHYLATION (MONO-) (PARTIAL).
DF51D490 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 49255 / MT4;
MEDLINE, 92062095.
BIROLO L., ARNONE M.I., CUBELLIS M.V., ANDREOTTI G., NITTI MARINO G., SANNIA G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 394; DB 1; Length 401;
Pred. No. 1.09e-55;
                                                                                                                                                                         SEQUENCE OF 1-22.
STRAIN=ATCC 49255 / MT4;
MEDLINE; 88315018.
MARINO G., NITTI G., ARNONE M.I., SANNIA G., GAMBACORTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.2%; Score 394; DB 1; Le Best Local Similarity 24.7%; Pred. No. 1.09e-55; Matches 96; Conservative 118; Mismatches 153;
                                                                                                                    spectrometry.";
EUR. J. BIOCHEM. 222:761-767(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16505; G809765; -.
STRAIN-ATCC 49255 / MT4; MEDLINE; 94298815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S07088; S07088.
S18362; S18362.
S21189; S21189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
202
384
401 AA;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 239-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-GLUTAMATE
                                                                                                             spectrometry
                                                                                                                                                                                                                                                                    ROSA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANNE J.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANNE J.D.,
KERLAYAGE A.R., DOUGHERTY B.A., TONB J.F., ADAMS M.D., RELOR C.I.,
OVERBEEK R., KIRNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.K., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ASEALMLSIMTLIDR-GDEVLIPNPSFVSYFSLTEFAEGKIKNIDL--DENFNIDLEKVK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 PAFRTAVEAEDAVAAALRIGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG 151
254 V-AKREIIQK--MGI-LAA--NVYTAPTSFVQKAAVKAFD-TFDEV-NQMVSLFKKRRDV 305
                                                MYDELIKVKGVEVS-KPNGAFYMFPNVSKILKTSGFDVKSLAIKLIEEKGVVTIPGEVFP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALYTIC ACTIVITY: L.ASPARTATE + 2-OXOGLUTARATE - OXALOACETATE L-GLUTAMATE (BY SIMILARITY)
-:- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \hat{A}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 PDFDTPKHIIEAAKRALDEGKTH-YSPNNGIPELREEISNKLKDDYNLDVDKDNIIVTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
42395 MW; 166A9EFC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Õ1-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDORATION UPDATE)
PUTATIVE ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.41e-50;
84; Mismatches 117; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM: PF00155; aminotran_1: 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 223 223 PYRIDOXAL PHOSPHATE (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 368;
                                                                                                                                                                                                                                                                                                                                                                      LGMEN-WVRITFACVPSSLQDGLERVKSF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
                                                                                                                                                                                                                                                                                               LNIGKEFLRLSFAVNEEVIKEGIQKIREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.4%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67459; G1592252; -.
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es 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHANOCOCCUS.
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PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG 151

AKHVLYTLFQVILN-EGDEVIIPIPYWVSYPEQVKLAG-GVPVYIEATSEQNYKITAEQL GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHF-DLIPDKGWEIDIDSL

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KNAITDK-TKAVIINSPSNPTGMVYTREELEDIAKIALENNILIVSDEIYEKLLYNGAEH 217 FSIAQISEEVKAQTIVINGVSKSHSMTGWRIGYAAG-NADIINAMTDLASHSTSNPTTAS 276 277 QYAA-I-EAY-NGPQDSVEEMRKAFESRL-ET--I-YPKLSAIPGFKVV-KPQGAFYLLP 328

FIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST

RF 390 448

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447 SF

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329 DVSEAAQKIGFASVDEFASALLIEANVAVIPGSGFGAPSTIRISYATSLNLIEEAIERID

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US-09-026-400-2.rsp

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GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAFNKLEVRHFDLIPDKGWEIDIDSL- 210
                                                         208 PMQ-FTDRC-IL-INGFSKTYAMTGWRIGYLAVSDELNKELDLINNMIKIHQY-SFAC-A 262
                                                                                                                                HIROTSU K., OKAMOTO A., HIGUCHI T., SODA K.;
"Thermostable aspartate aminotransferase from a thermophilic Bacillus
species. Gene cloning, sequence determination, and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and characterization of thermostable aspartate aminotransferase from a thermophilic Bacillus species.";
J. BACTERIOL. 172:1345-1351(1990).
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS. SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                              263 TIFAQYGALA-ALRGSQ-KCVEDMVREFKMRRDLIYNGLKDI-FKV--NKPDGAFYI 314
                                                                                                                                                                                                            330 ATFVQ-EALPKILENTKADFFKKIIGLKESSEICYREIKENKYITCPHKPEGSMFV 385
                                    ESIT-KKTKLIIFNSPSNPTGKVYDKETIKGLAEIAEDYNLIIVSDEVYDKIIYDKKHYS
                                                                                                                                                                                                                                                                                                                                           01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
8ASPARTATE AMINOTANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
BACILLUS SP. (STRAIN YM-2).
BACILLUS, FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91115885.
SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFERASE; AMINOTRANSFERASE; PVRIDOXAL PHOSPHATE.
BINDING
239 PYRIDOXAL PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> L (IN REF. 2).
8F0EC6D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 358; DB 1; 1
larity 23.5%; Pred. No. 4.28e-48;
Conservative 105; Mismatches 154
                                                                                                                                                                                                                                                                                             392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A38621; A38621.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOL. CHEM. 266:2567-2572(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: PYRIDOXAL PHOSPHATE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                     AAT_BACSP STANDARD; F P23034; 01-NOV-1991 (REL. 20, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-24 AND 387-392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M59430; G142538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91115885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization
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01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).

393 AA

PRT;

STANDARD:

AAT_BACST

BACILLUS STEAROTHERMOPHILUS. BACIERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.

SEQUENCE FROM N.A. STRAIN=ATCC 12980; MEDLINE; 96434469

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PRAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 237 237 27 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 393 AA; 42401 MW; 649AD162 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.22e-45;
.04; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 345; DB 1; I
23.8%; Pred. No. 2.22e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X93600; E212847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 86; Conserv
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42 PDFNTPQNIMDAAIDSMQQG-YTKYTPSGGLPALKQAIIEKFKRDNQLEYKPNEIIVGVG 100

105; Mismatches 154; Indels 18;

85.

-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE

L-GLUTAMATE.

BARTSCH K., SCHNEIDER R., SCHULZ A.;
Stereospecific production of the herbicide phosphinothricin (glufosinate): purification of aspartate transaminase from Bacill stearothermophilus, cloning of the corresponding gene, aspC, and application in a coupled transaminase process.";
APPL. ENVIRON. MCROBIOL. 62:3794-3799[1965].

Bacillus

-1- COFACTOR: PYRIDOXAL PHOSPHATE. -!- SUBUNIT: HOMODIMER (BY SIMILARITY). -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

AMINOTRANSFERASES.

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Query Match
Best Local Si
Matches 85
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                                                                                                                                  156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 KL-NLHLLEEIHDDIDFCCKLAKESVILCPGSVLGMENWVRITFACVPSSLQDGLERVK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the Bacillus subtilis chromosome region between
                                                                    151
         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the serA and kdg loci cloned in a yeast artificial chromosome.";
MICROBIOLOGY 142:2005-2016(1996).
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- COFACTOR: PYRIDOXAL PHOSPHATE.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (BY SIMILARITY). 930F37D6 CRC32;
                                                                                                                                                                             : :|: :: || : | ::::| | : | : : : : : | | : | CTQAIEVIIPVLAQTAGANILLLPREGYPNYEARAAFNKLEVRHF-DLIPDKGWEIDIDSL
                                                                                                                                                                                                                                                                                                                      211 -ESIADKNITAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPF
                                                                                                                                                                                                                                                                                                                                                                                 VSIAELSPELKAQTVIINGVSKSHSMTGWRIGYAA+-GPKDII-KA-M-TDLASH-STS-
                                                                                                                                                                                                                                                                                                                                                                                                                            270 IPMGVFG-HI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPTSIAQYAAIAAYSGPQEPV-EQMRQAFEQRLNIIYDKLVQIPGFTCV-KPQGAFYLFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAREAAAMAGCRIVDEFVAALLEEAKVALVPGSGFGAPDNVRLSYATSLDALETAVERIH
         PDFNTPQHILDAAIKAMNEGHTK-YTPSGGLPALKEEIIKKFARDQGLDYEPAEVIVCVG
                                                                    PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG
                                                                                                                                  AKHALYTLFQVLLD-EGDEVIIPTPYWVSYPEQVKLAG-GVPVYVEGLEQNHFKITPEQL
                                                                                                                                                                                                                                                            KQAITPR-TKAVIINSPSNPTGMIYTAEELKALGEVCLAHGVLIVSDEIYEKLTYGGAKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L47709; G1146246; -.
EMBL; Z99115; E1183682; -.
SUBTILIST; BG11513; ASPB.
SUBTILIST; BG11513; AAPA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 AA.
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43088 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
58 / MARBURG;
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393 AA;
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MEDLINE; 96349105
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P53001;
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SEQUENCE
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                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 FIPMGVFG-HI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVS 326
                                                                                                                                                                                                                                     TGAKHALYTLEQVILD-EEDEVIIPTPYWVSYPEQVKLAGGKPVYVEGLEENHFKISPEQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 IDPATFVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVM 386
                                                                                                                                                                                                                                                                                                                                                      LKNAITEK-TKAIVINSPSNPTGVMYTEEELSALGEVCLEHDILIVSDEIYEKLTYGGKK 214
                                                             Gaps
                                                                                                                    40 PDFNTPQHIIDAAVRSMNEGHTK-YTPSGGLAELKNSIAEKFKRDQNIEYK-PSQ-IIVC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATONIEWSKI C., SAVELLI B., STRACIER P.;
"The spoil gene, which regulates early developmental steps in
"The subtilis, belongs to a class of environmentally responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
-i- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                   150 AGGTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDS
                                                                                                                                                        L-ESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 -NPTSIAQYG-AIAAYNGPSEPLEEMREAFEHRLNTIYAKLIEIPGFSCV-KPEGAFYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNAKEAAQSCGFKDVDEFVKALLEEEKVAIVPGSGFGSPENVRLSYATSLDLLEEAIERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 HVSIAQLSDRLKEQTVIINGVSKSHSMTGWRIGYAA--GSEDII-KA-M-TNLASH-STS
                                                          20;
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Length 393;
10.2%; Score 330; DB 1; Length 393 tarity 23.2%; Pred. No. 2.86e-42; Conservative 117; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCANLAN E., DEVINE K.M.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AGG-1990 (REL. 15, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
10-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. BACTERIOL. 172:86-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 361-392 FROM N.A. 90094275.
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EMBL; Z99111; E1184990; -.
EMBL; M29450; G143632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                 Local Similarity
es 85: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS SUBTILIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSFCQRN 452
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P16524;
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
(EC. 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,

FAVELLO A., FULTON L., GATTING S., GRECO T., KIRSTEN J., KUCABA T.,

HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,

JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,

MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,

TACH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,

WILLSON R., WATERSTON R.;

SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                       108 LRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTA 167
                                                                                                                                                                                                                                                                                                                            112 GDEVIMPGPIYPGYEPIINLCGAKPVIVD-TTSHGFKLTARLIEDALTPNTKCVVLPYPS 170
                                                                                                                                                                                                                                                                                                                                                                168 GANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSLESIADKNTTAMYIINPN 227
                                                                                                                                                                                                                                                                                                                                                                                                     NPTGVTLSEBELKSIAALLKGRNVFVLSDEIYSELTYDRPHY-SIATYLRDQTIV-INGL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKSHSMTGWRIGFL--FAPKDI-AK-HI-LKVHQY-NVSCASSISQKAALEAVTNGLDDA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334
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                                                                                                                                                                             1 MEHLLNPKAREIEISGIR-KFSNLVAQHED--VISLTIGQPDFFTPHHVKAAAKKAIDEN 57
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    58 V-TS-YTP-NAGY-L-ELRQAVQLYMKKKADFNYDAESEIIITTGAQAIDAAFRTIL-SP
                                                                                                                                                                                                                                                                                                                                                                                                                            283 LIMR--EQYKKRLDYVY-DRLVSMGLDVV-KPSGAFYIFPSIK-SF--GM-TSFDFSNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 SKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 FFKRIIGLIKESSEICYREIKENKYIICPHKPEGSMFVMVKLNLHLLEEIHDDIDFCCKL
             PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 230 230 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 392 AA; 43414 MW; 8998A4D38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANSORGE W., VOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 LEDAGVALVPGSSFSTYGEGYVRLSFACSMDTLREGLDRLELFVLKKREAMQTIN 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERVILCEGSVIGM--ENWVRITFACVPSSLQDGLERVKSFCQRNKK-KNSIN 459
                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
BENES V., RECHMANN S., NENTWICH U., SCHWAGER C., ANSOKGE W., SUBMITTED (MAY-1996) TO EMBL/CENBANK/DDBJ DATA BANKS.
                                                                                                             Length 392;
                                                                                                        Score 301; DB 1; Length 392
Pred. No. 2.51e-36;
102; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-GLUTAMATE.
--- COFACTOR: PYRIDOXAL PHOSPHATE.
--- SUBCELLULAR LOCATION: MITOCHONDRIAL (POTENTIAL).
--- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                         Match 9.3%;
Local Similarity 23.4%;
les 97; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD:
 BG10205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLR089C OR L9449.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 2.6.1.2)
TRANSAMINASE)
 SUBTILIST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALAM_YEAST
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       171
                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 YSSSQGVEGIRKSVAEFITKRDEGEISYPEDIFLTAGASAAVNYLLSIFCRGPETGVLIP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 IPQYPLYTATLALNNSQALPYYLDENSGWSTNPEEIETVVKEAIQNEIKPTVLVVINPGN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLUTAMIC - - PYRUVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRIDOXAL PHOSPHATE (BY SIMILARITY). 5FF91EE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRIDOXAL PHOSPHATE (BY SIMILARITY) 5769BA88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE ALANINE AMINOTRANSFERASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŚEĞUENCE FROM N.A.
STRAIN-S288C / AB972;
MURPHY L., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLUTARATE - PYRUVATE L-GLUTAMATE.

L-GLUTAMATE.

-i - COFACTOR: PYRIDOXAL PHOSPHARIC (POTENTIAL).

-i - SUBCELLUTAR LOCATION: CYTOPLASMIC (POTENTIAL).

-i - SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                            EMBL; 273261; E245543; -.
EMBL; 273261; E245543; -.
HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
HYPOTHETICAL PROPERLY; MITOCHONDRION (POTENTIAL).
PYRIDORAL PHOSPHATE; MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIGAVLSPESIAQIFEVAAKYGTVVIADEVYQENIFPGTKFHSM 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE ALANINE MINOTRANSFERASE (EC 2.6.1.2) (GLUT
TRANSAMINASE) (GFT) (GLUTAMIC-*ALANINE TRANSAMINASE)
YDRILLC N YD9727.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.00e-
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56769 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.9%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 4
592 AA;
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BINDING 327 3
SEQUENCE 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAT_YEAST
P52892;
                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
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      SHEFF WWW NOCCO
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                                  6
                                                                                            218
                                                                                                                                                                                                                                   198 IPDKGWEIDIDSLESIA-D--KN---TTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGI 251
                                                                      100 ILRVGHNELASLNLFSRDALERAERLLNDI-GGSIGAYSHSQGVPGIRQTVADFITRRDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILIE; 93209934.

WATSON R. J., RASTOGI V.K.;

"Cloning and nucleotide sequencing of Rhizobium meliloti
"Cloning and nucleotide sequencing of shizobium meliloti
aminotransferase genes: an aspartate aminotransferase required for symbiotic nitrogen fixation is atypical.";
J. BACTERIOL. 175:1919-1928(1993).
-i. FUNCTION: REQUIRED FOR SYMBIOTIC NITROGEN FIXATION.
-i. CATALITIC ACTIVITY: L.ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RASTOGI V.K., WATSON R.J.; ASTOGI V.K., WATSON R.J.; Aspartate aminotransferase activity is required for aspartate catabolism and symbiotic nitrogen fixation in Rhizobium meliloti."; J. BACTERIOL. 173:2879-2887(1991).
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (REL. 26, CREATED)
1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-EEB-1995 (REL. 31, LAST ANOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE A (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; LUDSUCH; V. C. C. EMBL; LUDSUCH; A47094; A47094. A77094. PROSITE; PROOIUS; PA_TRANSFER_CLASS_1; 1. PROSITE; PS00105; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE. TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE (BY SIMILARITY). BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                              159 GEPATPEDIYLTTGASSAATSLLSLLCKDSQTGLLIPIPQYPLYTASASLFNAQVLPYYL
                                                                                                                                                                   DEESNWSTNSDEIEKVVQDALKKQIRPSVLIVINPGNPTGAVLSEETIARICLIAAKYGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
RHIZOBIACEAE; SINORHIZOBIUM.
                                     .
6
 Length 507;
                                    Indels
Score 294; DB 1;
Pred. No. 6.58e-35;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                400 AA
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                     61;
                                                                                                                                                                                                                                                                                                                 252 LVIADEVYGKLVLGSAPFIPM 272
                                                                                                                                                                                                                                                                                          279 TIISDEVYQENIFNDVKFHSM 299
 9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L05064; G152149; -.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIUM MELILOTI.
BACTERIA; PROTEOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91210178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JJ1C10;
                                       54;
                                                                                                                                                                                                                                                                                                                                                                                                  AATA_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                      219
                                                                                                                                                                                    138
                                         Matches
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Length 400;

DB 1;

8.8%; Score 285;

Query Match

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               24;
                                                                                                                                                                                                                                                                                                                                                                                         86 NLDYTAAQTIVGTGGKQILFNAFMATLN--PGDEVVIPAPYWVSYPEMVALCG-GTPVFV 142
                                                                                                                            PTRQENNFKLKAEDLDRAITPKTKWFVFNSPSNPSGAAYSHEELKALTDVLMKHPHVWVL 202
                                                                   31 RDVIGLGAGEPD-FDT-PDNIK-KAAIDAIDR-GETK-YTPVSGIPELREAIAKKFKREN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
               Gaps
                                                                                                                                                                                                                                                                                                                              TRISTSTIUVLNVSTDPATFVQEALPKILENTKADFFKRIIGLKESSEICYREIKENKY
                                                                                                                                                                                                                                                           260 A-MDM-IQG-QQTS-GAASIAQWAAVEALNGPQ-DFIGRNKEIFQGRRDLVVSMLNQAKG
                                                                                                                                                                                            203 IDDMYEHLTYGDFRFATPVEVEPGLYERILIMNGVSKAYAMTGWRIGYAA--GPLH-LIK
                                                                                                                                                                                                                                                                                                                                                                     ISCP-TPEGAFYVYPSCAGLIGKTAPSGKVIETDEDFVSELLETEGVAVVHGSAFGLGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35) LAST ANNOTATION UPDATE)
HYPOTHETICAL AMINOTABLEBASE TJL060W (EC 2.6.1.-).
YJL060W OK J1138.
SACCHARONCES CERENTIALS (BAKER'S YEAST).
EUKARYOTA, FUNGI: ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
               28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOKOYAMA K.,
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
POHL T.M., ALJINOVIC G.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
. No. 4.29e-33;
Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 AA
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LAST ANNOTATION UPDAT
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EMBL; D44603; G871966; -.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
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 Pred.
86; M
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(REL. 32, LAST SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 VRITFACVPSSLQDGLERVKSFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 92-222 FROM N.A.
 Best Local Similarity 24.5%;
Matches 94; Conservative
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MEDLINE; 95400292.
MURAKAMI Y., NAITOU M.
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P47039;
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277 IVLLADEVY

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                                                                                                                                                            184 WIIDFEQFEKAITSKTKAVIINTPHNPIGKVFTREELTILGNICVKHNVVIISDEVYEHL 243
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                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
01-0T-1996 (REL. 34, LAST ANNOTATION PEDATE)
PUTATIVE ALANINE AMIOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                  PYRIDOXAL PHOSPHATE (BY SIMILARITY)
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Pred. No. 3.91e-27;
49; Mismatches 75; Indels
                                                                                     Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL). SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
                                                                                     Score 258; DB 1; Length 444
Pred. No. 1.01e-27;
32; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLUTARATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 269909; E225673; -.
PFAM; PF00155; aminotran_1; 1.
HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
HYPOTHETICAL PROTEIN; AMINOTRANSFERASE; TRANSFERASE;
                                                                                                                                                                                                                                                         263 VLGSAPFIPMGVFG-HIADV-LSIGSLSKSWIVPGWRLGWV 301
                                                                                                                                                                                                                                  244 YF-TDSFTRIATLSPEIGQLTLTVGSAGKSFAATGWRIGWV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8CD487CF CRC32;
                                                  444 AA; 50082 MW; 16A5EF3D CRC32
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                                                                                                                                                                                                                                                                                                                                            505
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505 AA; 56627 MW;
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Local Similarity 28.6%;
                                                                                     Query Match 8.0%;
Best Local Similarity 32.7%;
Matches 33; Conservative
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                   PYRIDOXAL PHOSPHATE
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ALAT_SCHPO
Q10334;
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                                                    SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 SLESIADKNITAMVIINPNNPCGSVYSYDHLAKVAEVARKLG-ILVIADEVYGKLVLGSA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=104A14;
MEDLINE; 93308098.
ALFANO J.R., KAHN M.L.;
ALFANO J.R., KAHN M.L.;

"Isolation and characterization of a gene coding for a novel aspartate aminotransferase from Rhizobium meliloti.";

J. BACTERIOL. 175:4186-4196(1993).

-!- PUNCTION: INVOLVED IN SYMBIOTIC NITROGEN FIXATION.

L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
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JT 15
ATABLERIME STANDARD; PRT; 410 AA.
006191;
01-FEB-1994 (REL. 28, LAST ARDQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ARDQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ARDQUENCE UPDATE)
ASPARTATE AMINOTRANSFERASE B (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
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PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.

PFAM; PF00155; aminotran_1; 1.

TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.

BINDING 249 249

PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                       RHIZOBIUM MELLICTI.
BACTERIA; PROTECBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.5%; Score 241; DB 1; Length 410; Best Local Similarity 21.0%; Pred. No. 2.09e-24; Matches 77; Conservative 100; Mismatches 174; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                         RHIZOBIACEAE; SINORHIZOBIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L12149; G152151; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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